

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 11:04:00 ; Search time 192 Seconds
(without alignments)
62.932 Million cell updates/sec

Title: US-09-487-790A-1
Perfect score: 116
Sequence: 1 KGSWSMRKMSMKIRPFPPQ 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : Uniprot_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	491	1 FIBB_HUMAN	P02675 homo sapien
2	113	97.4	30	Q9N1E1	Q9n1e1 pan troglod
3	113	97.4	481	Q8K0E8	Q8k0e8 mus musculu
4	106	91.4	479	1 FIBB_RAT	P1480 rattus norv
5	103	88.8	468	1 FIBB_BOVIN	P02676 bos taurus
6	97	83.6	463	1 FIBB_CHICK	Q02020 gallus gall
7	85	73.3	485	2 Q6NVE1	Q6nve1 brachydanio
8	85	73.3	485	2 AAH66629	AAH66629 brachydan
9	83	71.6	477	1 FIBB_PETMA	P02678 petromyzon
10	82	70.7	321	2 Q7SVN8	Q7svn8 xenopus lae
11	82	70.7	488	2 Q91589	Q91589 xenopus lae
12	60	51.7	399	2 Q7Z664	Q7z664 homo sapien
13	60	51.7	437	2 AAP35744	AAP35744 homo sapi
14	60	51.7	453	1 FIBG_HUMAN	P02679 homo sapien
15	58	50.0	270	2 Q91332	Q91332 rana sylvat
16	58	50.0	316	2 Q28529	Q28529 mustela put
17	58	50.0	435	2 Q93568	Q93568 gallus gall
18	58	50.0	436	2 Q8VCW7	Q8vcw7 mus musculu
19	56	48.3	312	1 FGL1_HUMAN	Q08830 homo sapien
20	56	48.3	312	2 Q8NG32	Q8ng32 homo sapien
21	56	48.3	312	2 AAP35281	AAP35281 homo sapi
22	56	48.3	314	2 Q71KU9	Q71ku9 mus musculu
23	56	48.3	314	2 Q8VC25	Q8vc25 mus musculu
24	56	48.3	314	2 AAQ05798	AAQ05798 mus muscu
25	56	48.3	444	1 FIBG_BOVIN	P12799 bos taurus
26	56	48.3	445	1 FIBG_RAT	P02680 rattus norv
27	52	44.8	346	2 Q43827	Q43827 homo sapien
28	52	44.8	346	2 AAQ88668	AAQ88668 homo sapi
29	51	44.0	235	2 Q28763	Q28763 papio cynoc
30	51	44.0	438	1 FIBG_XENLA	P17634 xenopus lae
31	51	44.0	866	1 FIBB_HUMAN	P02671 homo sapien

32	51	44.0	1643	2	Q8NL80	Q8nl80 corynebacte
33	51	44.0	1646	2	Q6M1E9	Q6m1e9 corynebacte
34	51	44.0	1646	2	CAF19007	CAF19007 corynebacte
35	50	43.1	439	2	Q7SZ13	Q7sz13 xenopus lae
36	50	43.1	782	2	Q7TQ70	Q7tq70 rattus norv
37	50	43.1	910	2	Q8VWV9	Q8vwv9 pinus pinas
38	49.5	42.7	145	2	Q901F9	Q901f9 human immun
39	49	42.2	236	2	Q912P1	Q912p1 mus musculu
40	49	42.2	343	2	Q7ZX13	Q7zx13 xenopus lae
41	49	42.2	1725	2	Q80U46	Q80u46 mus musculu
42	49	42.2	1960	1	TF20_HUMAN	TF20_HUMAN
43	49	42.2	1983	1	TF20_MOUSE	TF20_MOUSE
44	48	41.4	313	2	Q6G1L5	Q6g1l5 xenopus lae
45	48	41.4	343	2	Q6DJE9	Q6dje9 xenopus lae
46	47.5	40.9	128	1	RNP4_METJA	RNP4_METJA
47	47	40.5	125	2	O59042	O59042 pyrococcus
48	47	40.5	244	2	Q9HBP3	Q9hbp3 homo sapien
49	47	40.5	308	2	Q7PZN3	Q7pzn3 anopheles g
50	47	40.5	310	2	Q7QNI7	Q7qni7 anopheles g
51	47	40.5	337	2	Q8RIQ3	Q8riq3 mus musculu
52	47	40.5	375	1	AGP2_BOVIN	AGP2_BOVIN
53	47	40.5	407	2	Q9PU54	Q9pu54 gallus gall
54	47	40.5	407	2	Q9DER1	Q9der1 gallus gall
55	47	40.5	441	2	Q9DER0	Q9der0 gallus gall
56	47	40.5	470	2	Q8NI99	Q8ni99 homo sapien
57	47	40.5	470	2	Q9BZ20	Q9bz20 homo sapien
58	47	40.5	470	2	AAQ88643	AAQ88643 homo sapi
59	47	40.5	493	2	Q9DER2	Q9der2 gallus gall
60	47	40.5	496	1	AGP2_HUMAN	AGP2_HUMAN
61	47	40.5	496	1	AGP2_MOUSE	AGP2_MOUSE
62	47	40.5	496	1	AGP2_PIG	AGP2_PIG
63	46.5	40.1	205	2	Q6IUE1	Q6iue1 human immun
64	46	39.7	43	2	Q8MIK6	Q8mik6 macaca mula
65	46	39.7	115	2	O06371	O06371 mycobacteri

ALIGNMENTS

RESULT 1	FIBB_HUMAN	STANDARD;	PRT;	491 AA.
ID	FIBB_HUMAN	STANDARD;	PRT;	491 AA.
AC	P02675;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].			
GN	Name=FGB;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=91344740; PubMed=2102623;			
RA	Chung D.W., Harris J.E., Davie E.W.;			
RT	"Nucleotide sequences of the three genes coding for human			
RT	fibrinogen.";			
RL	Adv. Exp. Med. Biol. 281:39-48(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=83283433; PubMed=6688356;			
RA	Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;			
RT	"Characterization of complementary deoxyribonucleic acid and genomic			
RT	deoxyribonucleic acid for the beta chain of human fibrinogen.";			
RL	Biochemistry 22:3244-3250(1983).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Chung D.W., Harris J.E., Davie E.W.;			
RT	"Nucleotide sequences of the three genes coding for human			
RT	fibrinogen.";			
RL	(in) Liu C.Y., Chien S. (eds.);			
RL	Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48, Plenum			

RL Press, New York (1991).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS SER-100; HIS-170; LEU-265 AND
RP LYS-478.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNP. NHLBI HL66682 program for genomic applications, UW-
RT FRCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT structural variants.";
RL (in) Peters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL Pergamon Press, Oxford (1980).
RN [6]
RP SEQUENCE OF 31-491.
RX MEDLINE=79124640; PubMed=420779;
RA Watt K.W.K., Takagi T., Doolittle R.F.;
RT "Amino acid sequence of the beta chain of human fibrinogen.";
RL Biochemistry 18:68-76(1979).
RN [7]
RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
RX MEDLINE=76225080; PubMed=936108;
RA Blombaeck B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL Thromb. Res. 8:639-658(1976).
RN [8]
RP SEQUENCE OF 1-38 FROM N.A.
RX MEDLINE=87146483; PubMed=3029722;
RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
RA Marguerie G.;
RT "Characterization of the 5'-flanking region for the human fibrinogen
RT beta gene.";
RL Nucleic Acids Res. 15:1615-1625(1987).
RN [9]
RP SEQUENCE OF 31-44.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
RN [10]
RP REVIEW, AND DISULFIDE BONDS.
RX MEDLINE=83254370; PubMed=6575689;
RA Henschen A., Lottspeich F., Kehl M., Southan C.;
RT "Covalent structure of fibrinogen.";
RL Ann. N. Y. Acad. Sci. 408:28-43(1983).
RN [11]
RP DISULFIDE BONDS.
RX MEDLINE=77245999; PubMed=891553;
RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blombaeck B.;
RT "Primary structure of human fibrinogen. Characterization of disulfide-
RT containing cyanogen-bromide fragments.";
RL Eur. J. Biochem. 77:595-610(1977).
RN [12]
RP DISULFIDE BONDS.
RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Frieze S.J.;
RT "The structures of fibrinogen and fibrin.";
RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K., Neurath H.
RL (eds.);
RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
RL Pergamon Press, New York (1978).
RN [13]
RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RT "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
RX MEDLINE=97472408; PubMed=9333233;

RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
RT crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RT different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [16]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL Biochemistry 38:2941-2946(1999).
RN [17]
RP INTERACTION WITH FBLN1.
RX MEDLINE=95370284; PubMed=7642629;
RA Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
RA Argaves W.S.;
RT "The interaction of fibulin-1 with fibrinogen. A potential role in
RT hemostasis and thrombosis.";
RL J. Biol. Chem. 270:19458-19464(1995).
RN [18]
RP VARIANT BALTIMORE-2 LYS-478.
RX MEDLINE=89058942; PubMed=3194892;
RA Schmelzer C.H., Ebert R.F., Bell W.R.;
RT "A polymorphism at B beta 448 of fibrinogen identified during
RT structural studies of fibrinogen Baltimore II.";
RL Thromb. Res. 52:173-177(1988).
RN [19]
RP VARIANT ISE ARG-45.
RX MEDLINE=91208409; PubMed=2018836;
RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yanazumi K.,
RA Asakura S., Shirakawa S.;
RT "A new congenital abnormal fibrinogen Ise characterized by the
RT replacement of B beta glycine-15 by cysteine.";
RL Blood 77:1958-1963(1991).
RN [20]
RP VARIANT NAPLES THR-98.
RX MEDLINE=92340664; PubMed=1634610;
RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
RT "Molecular basis of fibrinogen Naples associated with defective
RT thrombin binding and thrombophilia. Homozygous substitution of B beta
RT 68 Ala-->Thr.";
RL J. Clin. Invest. 90:238-244(1992).
RN [21]
RP VARIANTS IJMUUDEN CYS-44 AND NIJMEGEN CYS-74.
RX MEDLINE=92228809; PubMed=1565641;
RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
RA Kerst A.P.J.A., Lord S.T.;
RT "Abnormal fibrinogens IJmuuden (B beta Arg14-->Cys) and Nijmegen (B
RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
RT complexes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
RN [22]
RP VARIANT NEW YORK-1 39-GLY--LEU-102 DEL.
RX MEDLINE=85157605; PubMed=3156856;
RA Liu C.Y., Koehn J.A., Morgan F.J.;
RT "Characterization of fibrinogen New York 1. A dysfunctional fibrinogen
RT with a deletion of B beta(9-72) corresponding exactly to exon 2 of the
RT gene.";
RL J. Biol. Chem. 260:4390-4396(1985).
RN [23]
RP VARIANTS GLU-2; LEU-265 AND LYS-478.
RX MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,
RA Lander E.S.;

RT "Characterization of single-nucleotide polymorphisms in coding regions
 of human genes.";
 RL Nat. Genet. 22:231-238 (1999).
 RN [24]

RP ERRATUM.
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.P., Lim E.P., Kalyanaram N., Nemes J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RL Nat. Genet. 23:373-373 (1999).
 RN [25]

RN VARIANTS CONGENITAL AFIBRINOGENEMIA ARG-383 AND ASP-430.

RX MEDLINE=20129589; PubMed=10666208;

RA Duga S., Asselta R., Santagostino E., Zeinali S., Simonic T.,

RA Malcovati M., Mannucci P.M., Turchini M.L.;

RT "Missense mutations in the human beta fibrinogen gene cause congenital
 afibrinogenemia by impairing fibrinogen secretion.";
 RL Blood 95:1336-1341 (2000).
 RN [26]

RN VARIANT CONGENITAL AFIBRINOGENEMIA CYS-196.

RX MEDLINE=21361164; PubMed=11468164;

RA Lounes K.C., Lefkowitz J.B., Henschen-Edman A.H., Coates A.I.,

Query Match 100.0%; Score 116; DB 1; Length 491;

Best Local Similarity 100.0%; Pred. No. 3.3e-10;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSKIRPFPPQ 21

Db 471 KGSWYSMRKMSKIRPFPPQ 491

|||||:|||||:|||||:|||||

RESULT 2

ID Q9N1E1 PRELIMINARY; PRT; 30 AA.

AC Q9N1E1;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Beta-fibrinogen (Fragment).

GN Name=Beta-fibrinogen;

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

OX NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RA Rupert J.L., Hochachka P.W.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF200356; AAF66219.1; -

DR InterPro; IPR002181; Fibrinogen_C.

DR Pfam; PF00147; Fibrinogen_C; 1.

FT NON_TER 1

SQ SEQUENCE 30 AA; 3709 MW; 89105BDC9C4FCB89 CRC64;

Query Match 97.4%; Score 113; DB 2; Length 30;

Best Local Similarity 95.2%; Pred. No. 5e-11;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSKIRPFPPQ 21

Db 10 KGSWYSMRKMSKIRPFPPQ 30

|||||:|||||:|||||:|||||

RESULT 3

ID Q8K0E8 PRELIMINARY; PRT; 481 AA.

AC Q8K0E8;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Fibrinogen, B beta polypeptide.

GN Name=Fgb;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=FVB/N; TISSUE=Liver;

RC MEDLINE=223388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Tohbiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN=FVB/N; TISSUE=Liver;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC031715; AAH31715.1; -

DR HSSP; P02675; IFZE.

DR MGD; MGI:99501; Fgb.

DR InterPro; IPR002181; Fibrinogen_C.

DR Pfam; PF00147; Fibrinogen_C; 1.

DR SMART; SM00186; Fbg; 1.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

SQ SEQUENCE 481 AA; 54752 MW; 9902830CF708A155 CRC64;

Query Match 97.4%; Score 113; DB 2; Length 481;

Best Local Similarity 95.2%; Pred. No. 9.9e-10;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSKIRPFPPQ 21

Db 461 KGSWYSMRKMSKIRPFPPQ 481

|||||:|||||:|||||:|||||

RESULT 4

ID FIBB_RAT

AC F1480;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].

GN Name=Fgb;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=Sprague-Dawley; TISSUE=Liver;

RC MEDLINE=95143386; PubMed=7841303;

RA Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.;

RA "Cloning of the complete coding sequence of rat fibrinogen B beta

chain cDNA: interspecies conservation of fibrin beta 15-42 primary

structure.";

RT Blood Coagul. Fibrinolysis 5:487-496 (1994).
 RL

RN [2]
 RP SEQUENCE OF 1-26 FROM N.A.
 RA MEDLINE=84194000; PubMed=6232608;
 RX Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
 RT "Potential basis for regulation of the coordinately expressed
 RL fibrinogen genes: homology in the 5' flanking regions.";
 RN Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
 RN [3]
 RP SEQUENCE OF 19-32.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [4]
 RP SEQUENCE OF 183-479 FROM N.A.
 RA MEDLINE=89378771; PubMed=2673932;
 RX Eastman E.M., Gilula N.B.;
 RT "Cloning and characterization of a cDNA for the B beta chain of rat
 RL fibrinogen: evolutionary conservation of translated and 3'-
 RT untranslated sequences.";
 RN Gene 79:151-158(1989).
 RN [5]
 RP SEQUENCE OF 425-479 FROM N.A.
 RA STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=87134033; PubMed=3817019;
 RA Sobczak J., Lotfi A.-M., Taroux P., Duguet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 RL liver regeneration.";
 RN Exp. Cell Res. 169:47-56(1987).
 CC -1- FUNCTION: Fibrinogen has a double function: Yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 CC (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL; U05675; AAA64866.1; -;
 DR EMBL; M27220; AAA41160.1; -;
 DR EMBL; K01336; AAA98625.1; -;
 DR EMBL; M35602; AAA41159.1; -;
 DR PIR; A05299; A05299.
 DR PIR; I67595; I67595.
 DR HSSP; P02675; 1PZE.
 DR RGD; 2604; Fgb.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C DOMAIN; 1.
 KW Blood coagulation; Direct protein sequencing; Glycoprotein; Plasma;
 KW Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 479 Fibrinogen beta chain.
 FT PEPTIDE 19 32 Fibrinopeptide B.
 FT DISULFID 211 211 Interchain (with alpha chain) (By
 FT similarity).
 FT DISULFID 215 215 Interchain (with gamma chain) (By
 FT similarity).
 FT DISULFID 219 304 By similarity.
 FT DISULFID 229 258 By similarity.
 FT DISULFID 412 425 By similarity.
 FT CARBOHYD 382 382 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 28 30 LSI -> ILS (in Ref. 3).

FT CONFLICT 439 439 L -> Q (in Ref. 5).
 FT CONFLICT 441 441 S -> T (in Ref. 5).
 FT CONFLICT 445 445 S -> A (in Ref. 5).
 FT CONFLICT 467 467 R -> K (in Ref. 5).
 FT CONFLICT 475 475 V -> F (in Ref. 5).
 SQ SEQUENCE 479 AA; 54303 MW; EC8C6DB77C3E05C0 CRC64;
 Query Match 91.4%; Score 106; DB 1; Length 479;
 Best Local Similarity 90.5%; Pred. No. 1.4e-08;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKSMKIRPFPPQQ 21
 DB 459 KGSWYSMRKSMKIRPFPPQQ 479
 RESULT 5
 FIBB_BOVIN STANDARD; PRT; 468 AA.
 ID FIBB_BOVIN
 AC P02676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN Name=FBG;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-4.
 RA Blomback B., Doolittle R.F.;
 RT "The sequence of amino acids at the N-terminal end of bovine
 RL fibrinopeptide B.";
 RN Acta Chem. Scand. 17:1816-1819(1963).
 RP SEQUENCE OF 5-21.
 RA Sjoquist J., Blomback B., Wallen P.;
 RT "Amino acid sequence of bovine fibrinopeptides.";
 RN Ark. Kemi 16:425-436(1960).
 RP SEQUENCE OF 22-53.
 RX MEDLINE=79164394; PubMed=434821;
 RA Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
 RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;
 RT "Amino acid sequences of portions of the alpha and beta chains of
 RL bovine fibrinogen.";
 RN Arch. Biochem. Biophys. 192:27-32(1979).
 RP SEQUENCE OF 44-468 FROM N.A.
 RX MEDLINE=81199473; PubMed=6262803;
 RA Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
 RT "Characterization of a cDNA clone coding for the beta chain of bovine
 RL fibrinogen."
 CC -1- FUNCTION: Fibrinogen has a double function: Yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 CC (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot. The soft clot is converted
 CC into the hard clot by factor XIIIa which catalyzes the epsilon-
 CC (gamma-glutamyl)lysine cross-linking between gamma chains
 CC (stronger) and between alpha chains (weaker) of different
 CC monomers.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC
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EMBL; V00110; CAA23444.1; -
PDB; 1DEQ; X-ray; B/E/O/R=61-468.
PDB; 1JY2; X-ray; O/R=61-116.
PDB; 1JY3; X-ray; O/R=61-116.
InterPro; IPR002181; Fibrinogen_C.
Pfam; SM00186; FBG; 1.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
3D-structure; Blood coagulation; Direct protein sequencing;
Glycoprotein; Plasma; Platelet; Pyrrolidone carboxylic acid;
Sulfation.
FT PEPTIDE 1 21 Fibrinopeptide B.
FT CHAIN 22 468 Fibrinogen beta chain.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 6 6 Sulfotyrosine.
FT SITE 21 22 Cleavage (by thrombin; release fibrinopeptide B).
FT DISULFID 72 72 Interchain (with alpha).
FT DISULFID 83 83 Interchain (with alpha).
FT DISULFID 87 87 Interchain (with alpha).
FT DISULFID 200 200 Interchain (with alpha).
FT DISULFID 204 204 Interchain (with alpha).
FT DISULFID 208 293 By similarity.
FT DISULFID 218 247 By similarity.
FT DISULFID 401 414 By similarity.
FT CARBOHYD 371 371 N-linked (GLCNAC. . .) (Probable).
FT STRAND 72 73
FT TURN 77 79
FT STRAND 81 84
FT HELIX 86 112
FT TURN 113 113
SQ SEQUENCE 468 AA; 53340 MW; 2DED42F443AA4B37 CRC64;

Query Match 88.8%; Score 103; DB 1; Length 468;
Best Local Similarity 81.0%; Pred. No. 4.1e-08;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFPPQ 21
:|||||:|||||:|||||:
Db 448 QGSWYSMKMSKIRPFPEQ 468

RESULT 6
FIBB_CHICK STANDARD; PRT; 463 AA.
AC Q02020;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
DE (Fragment).
GN Name=FBG;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archoosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE=91182745; PubMed=2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
RT cleavage site."
RL Biochemistry 30:3290-3294 (1991).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.

CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot. The soft clot is converted
CC into the hard clot by factor XIIIa which catalyzes the epsilon-
CC (gamma-glutamyl)lysine cross-linking between gamma chains
CC (stronger) and between alpha chains (weaker) of different
CC monomers.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC -----
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EMBL; M58514; AAA48770.1; -
PIR; A38463; A38463.
PDB; 1E13; X-ray; B/E=1-463.
PDB; 1MLJ; X-ray; B/E=1-463.
InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; Fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
3D-structure; Blood coagulation; Direct protein sequencing;
Glycoprotein; Plasma; Platelet; Sulfation.
NON_TER 1 1
FT PEPTIDE <1 17 Fibrinopeptide B.
FT CHAIN 18 463 Fibrinogen beta chain.
FT MOD_RES 5 5 Sulfotyrosine (By similarity).
FT SITE 17 18 Cleavage (by thrombin; release fibrinopeptide B).
FT DISULFID 69 69 Interchain (with alpha) (By similarity).
FT DISULFID 80 80 Interchain (with alpha) (By similarity).
FT DISULFID 84 84 Interchain (with gamma) (By similarity).
FT DISULFID 197 197 Interchain (with alpha) (By similarity).
FT DISULFID 201 201 Interchain (with gamma) (By similarity).
FT DISULFID 205 289 By similarity.
FT DISULFID 215 244 By similarity.
FT DISULFID 397 410 By similarity.
FT CARBOHYD 367 367 N-linked (GLCNAC. . .) (Potential).
SQ SEQUENCE 463 AA; 52678 MW; 204CD49BA79EC7B CRC64;

Query Match 83.6%; Score 97; DB 1; Length 463;
Best Local Similarity 84.2%; Pred. No. 3.9e-07;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFPP 19
:|||||:|||||:|||||:
Db 444 KGSWYSMKMSKIRPFPP 462

RESULT 7
Q6NYE1 PRELIMINARY; PRT; 485 AA.
AC Q6NYE1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein fgb.
GN Name=fgb;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;

```

RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066629; AAH66629.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
KW Hypothetical protein.
SQ SEQUENCE 485 AA; 54407 MW; A3622504448B0FF3 CRC64;

Query Match 73.3%; Score 85; DB 2; Length 485;
Best Local Similarity 66.7%; Pred. No. 3.7e-05;
Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPFPPQ 21
Db |||||: :|||||: |
465 KGSWYSLKTIISMKIRPFQOK 485

RESULT 9
FIBB_PETMA
ID FIBB_PETMA STANDARD; PRT; 477 AA.
AC P02678;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragments).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE OF 1-36.
RX MEDLINE=77065679; PubMed=999898;
RA Cottrell B.A., Doolittle R.F.;
RT "Amino acid sequences of lamprey fibrinopeptides A and B and
RT characterizations of the junctions split by lamprey and mammalian
RT thrombins.";
RL Biochim. Biophys. Acta 453:426-438 (1976).
RN [2]
RP SEQUENCE OF 37-477 FROM N.A.
RX MEDLINE=87076582; PubMed=3790537;
RA Bohonus V.L., Doolittle R.F., Pontes M., Strong D.D.;
RT "Complementary DNA sequence of lamprey fibrinogen beta chain.";
RL Biochemistry 25:6512-6516 (1986).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot. The soft clot is converted
CC into the hard clot by factor XIIIa which catalyzes the epsilon-
CC (gamma-glutamyl)lysine cross-linking between gamma chains
CC (stronger) and between alpha chains (weaker) of different
CC monomers.
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC -----
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RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054326; AAH54326.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 321 AA; 36519 MW; E0C41FCC3EB40DEF CRC64;

Query Match 70.7%; Score 82; DB 2; Length 321;
Best Local Similarity 77.8%; Pred. No. 7.3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFF 18
| | | | | : | | | | |
DB 303 KDSWYSMKMSIKIRPYF 320

RESULT 11
QY1589 PRELIMINARY; PRT; 488 AA.
ID Q91589
AC Q91589; Q91546;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibrinogen B-beta subunit precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9536963; PubMed=7642099;
RA Roberts L.R., Nichols L.A., Holland L.J.;
RT "cDNA and amino-acid sequences and organization of the gene encoding
RT the B beta subunit of fibrinogen from Xenopus laevis.";
RL Gene 160:223-228(1995).
DR EMBL; U19618; AAA85283.1; -.
DR PIR; A48810; A48810.
DR HSP; P02675; 1LTJ.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW SIGNAL.
FT CHAIN 1 16
FT CHAIN 17 43 B fibrinopeptide.
FT CHAIN 17 488 fibrinogen B-beta subunit.
SQ SEQUENCE 488 AA; 54803 MW; 660E03844B8C6414 CRC64;

Query Match 70.7%; Score 82; DB 2; Length 488;
Best Local Similarity 77.8%; Pred. No. 0.00011;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFF 18
| | | | | : | | | | |
DB 470 KDSWYSMKMSIKIRPYF 487

RESULT 12
QY2664 PRELIMINARY; PRT; 399 AA.
ID Q72664
AC Q72664;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKF2p779N0926 (Fragment).
GN Name=DKF2p779N0926;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538098; CAD98014.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 399 AA; 45092 MW; 9451321C29AB5C9A CRC64;

Query Match 51.7%; Score 60; DB 2; Length 399;
Best Local Similarity 64.7%; Pred. No. 0.36;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFF 17
| | | | | : | | | | |
DB 361 KTRWYSMKTTMKIIPF 377

RESULT 13
AAP35744 PRELIMINARY; PRT; 437 AA.
ID AAP35744
AC AAP35744;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibrinogen, gamma polypeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT007081; AAP35744.1; -.
SQ SEQUENCE 437 AA; 49496 MW; 3D73A7BC1E71381B CRC64;

Query Match 51.7%; Score 60; DB 2; Length 437;
Best Local Similarity 64.7%; Pred. No. 0.4;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFF 17
| | | | | : | | | | |
DB 399 KTRWYSMKTTMKIIPF 415

RESULT 14
FIBG HUMAN STANDARD; PRT; 453 AA.
ID FIBG HUMAN
AC P02679; P04469; P04470; Q96A14; Q96KJ3;
DT 21-JUL-1986 (Rel. 01, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen gamma chain precursor (PRO2061).
GN Name=FBG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
```

RX MEDLINE=85252774; PubMed=2990550;
 RA Rixon M.W., Chung D.W., Davie E.W.;
 RT "Nucleotide sequence of the gene for the gamma chain of human
 RT fibrinogen.";
 RL Biochemistry 24:2077-2086(1985).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=83283434; PubMed=6688357;
 RA Chung D.W., Chan W.-Y., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT the gamma chain of human fibrinogen.";
 RL Biochemistry 22:3250-3256(1983).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
 RP Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
 RT FHCC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RP TISSUE=Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
 RA He F.;
 RT "Functional prediction of the coding sequences of 33 new genes deduced
 RT by analysis of cDNA clones from human fetal liver.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RP TISSUE=Skeletal muscle;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RN SEQUENCE OF 27-437.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants.";
 RL (In) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [7]
 RN SEQUENCE OF 75-286 FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=92119334; PubMed=1685103;
 RA Marchetti L., Zanelli T., Malcovati M., Tencchini M.L.;
 RT "Polymorphism of the human gamma chain fibrinogen gene.";
 RL DNA Seq. 1:419-422(1991).
 RN [8]
 RN SEQUENCE OF 285-437 FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
 RP MEDLINE=85030379; PubMed=6092346;
 RA Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,
 RA Crabtree G.R.;
 RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing
 RT near the 3' end of the gene produces gamma A and gamma B forms of

gamma-fibrinogen.";
 RL J. Biol. Chem. 259:12826-12830(1984).
 RN [9]
 RN SEQUENCE OF 209-270 FROM N.A.
 RP MEDLINE=84069777; PubMed=6689067;
 RA Inam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
 RT "Isolation and characterisation of cDNA clones for the A alpha- and
 RT gamma-chains of human fibrinogen.";
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [10]
 RN SEQUENCE OF 411-453 (ISOFORM GAMMA-B).
 RP MEDLINE=82068993; PubMed=7306501;
 RA Wolfenstein-Todel C., Mosesson M.W.;
 RT "Carboxy-terminal amino acid sequence of a human fibrinogen gamma-
 RT chain variant [gamma'].";
 RL Biochemistry 20:6146-6149(1981).
 RN [11]
 RN REVIEW, AND DISULFIDE BONDS.
 RP MEDLINE=83254370; PubMed=6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N. Y. Acad. Sci. 408:28-43(1983).
 RN [12]
 RN DISULFIDE BONDS.
 RP Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K., Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [13]
 RN DISULFIDE BONDS.
 RP MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [14]
 RN QUATERNARY STRUCTURE, AND DISULFIDE BONDS.
 RP MEDLINE=83231485; PubMed=6860649;
 RA Hoepflich P.D., Doolittle R.F.;
 RT "Pimeric half-molecules of human fibrinogen are joined through
 RT disulfide bonds in an antiparallel orientation.";
 RL Biochemistry 22:2049-2055(1983).
 RN [15]
 RN SULFATION.
 RP MEDLINE=91369960; PubMed=1892842;
 RA Farrell D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;
 RT "Recombinant human fibrinogen and sulfation of the gamma' chain.";
 RL Biochemistry 30:9414-9420(1991).
 RN [16]
 RN REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RP MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [17]
 RN POLYMERIZATION SITE.
 RP MEDLINE=85014892; PubMed=6592597;
 RA Horwitz B.H., Varadi A., Scheraga H.A.;
 RT "Localization of a fibrin gamma-chain polymerization site within
 RT segment Thr-374 to Glu-396 of human fibrinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
 RN [18]
 RN POLYMERIZATION SITE.
 RP MEDLINE=81142375; PubMed=6451630;
 RA Olexa S.A., Budzynski A.Z.;
 RT "Localization of a fibrin polymerization site.";
 RL J. Biol. Chem. 256:3544-3549(1981).
 RN [19]
 RN PLATELET AGGREGATION SITE.
 RP MEDLINE=84203545; PubMed=6326808;
 RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;

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RT "Platelet receptor recognition site on human fibrinogen. Synthesis and
RT structure-function relationship of peptides corresponding to the
RT carboxy-terminal segment of the gamma chain."
RL Biochemistry 23:1767-1774 (1984).
[20]
RN PLATELET AGGREGATION SITE.
RP MEDLINE=84185664; PubMed=6325435;
RA Flow E.F., Srouji A.H., Meyer D., Marguerie G., Ginsberg M.H.;
RT "Evidence that three adhesive proteins interact with a common
RT recognition site on activated platelets."
J. Biol. Chem. 259:5388-5391 (1984).
[21]
RN CALCIUM-BINDING SITE.
RP MEDLINE=85261382; PubMed=3160702;
RA Dang C.V., Ebert R.F., Bell W.R.;
RT "Localization of a fibrinogen calcium binding site between gamma-
RT subunit positions 311 and 336 by terbium fluorescence."
J. Biol. Chem. 260:9713-9719 (1985).
[22]
RN CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
RP MEDLINE=81054908; PubMed=6933547;
RA Wolfenstein-Todel C., Moseson M.W.;
RT "Human plasma fibrinogen heterogeneity: evidence for an extended
RT carboxyl-terminal sequence in a normal gamma chain variant (gamma').";
Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073 (1980).
[23]
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
RP MEDLINE=97169449; PubMed=9016719;
RA Yee V.C., Pratt K.P., Core H.C.F., le Trong I., Chung D.W.,
RA Davie E.W., Stenkamp R.E., Teller D.C.;
RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma
RT chain of human fibrinogen."
Structure 5:125-138 (1997).
[24]
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
RP MEDLINE=97352771; PubMed=9207064;
RA Pratt K.P., Core H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;
RT "The primary fibrin polymerization pocket: three-dimensional structure
RT of a 30-kDa C-terminal gamma chain fragment complexed with the peptide
RT Gly-Pro-Arg-Pro."
Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181 (1997).
Query Match 51.7%; Score 60; DB 1; Length 453;
Best Local Similarity 64.7%; Pred. No. 0.41;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPF 17
Db 399 KTRWYSMKTKTKIIPF 415

RESULT 15
Q91332 ID Q91332 PRELIMINARY; PRT; 270 AA.
AC Q91332;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibrinogen gamma subunit (Fragment).
OS Rana sylvatica (Wood frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=45438;
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=97319437; PubMed=9176340;
RA Cai Q., Storey K.B.;
RT "Freezing-induced genes in wood frog (Rana sylvatica): fibrinogen
RT upregulation by freezing and dehydration."
Am. J. Physiol. 272:R1480-R1492 (1997).
RL EMBL; U44829; AAA97879.1; -.
DR InterPro; IPR002181; Fibrinogen_C.

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DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
FT NON_TER 1
SQ SEQUENCE 270 AA; 30878 MW; A780763F14288CFC CRC64;

Query Match 50.0%; Score 58; DB 2; Length 270;
Best Local Similarity 78.6%; Pred. No. 0.5;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
Db 236 WYSMRKMSMKIIPF 249

RESULT 16
Q28529 ID Q28529 PRELIMINARY; PRT; 316 AA.
AC Q28529;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibrinogen, gamma A chain (Fragment).
OS Mustela putorius (European polecat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=96144287; PubMed=8566791;
RA Simpson-Haidaris P.J., Wright T.W., Earnest B.J., Hui Z., Neroni L.A.,
RA Courtney M.A.;
RT "Cloning and characterization of a lung-specific cDNA corresponding to
RT the gamma chain of hepatic fibrinogen."
Gene 167:273-278 (1995).
RL EMBL; U28494; AAA96954.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 316 AA; 35733 MW; F91836C38EC3709A CRC64;

Query Match 50.0%; Score 58; DB 2; Length 316;
Best Local Similarity 71.4%; Pred. No. 0.6;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
Db 281 WYSMRKTKTKIIPF 294

RESULT 17
O93568 ID O93568 PRELIMINARY; PRT; 435 AA.
AC O93568;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibrinogen gamma chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Liver;
RA Cao Y., Weissbach L., Fu Y., Grieninger G.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087432; AAC36476.1; -.

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DR PDB; 1BI3; X-ray; C/F=27-435.
DR PDB; 1MIJ; X-ray; C/F=27-435.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR002181; Fibrinogen C.
DR InterPro; IPR008994; Fibrinogen C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 435 AA; 49642 MW; 91D2BC7F86850766 CRC64;

Query Match 50.0%; Score 58; DB 2; Length 435;
Best Local Similarity 58.8%; Pred. No. 0.84;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKSMKIRPF 17
DB 402 WYSMKTTMKIIPF 415
|||||:|||||

RESULT 18
Q8VCM7 ID Q8VCM7 PRELIMINARY; PRT; 436 AA.
AC Q8VCM7; Q8VUR3;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Fibrinogen, gamma polypeptide.
GN Name=Fgg;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver, and Salivary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Haieh F.,
RA Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Kerneran K.J., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver, and Salivary gland;
RX Submitted (DSC-2001) to the ENBL/GenBank/DBJ databases.
RL EMBL; BC019506; AAH19506.1; -.
DR EMBL; BC019828; AAH19828.1; -.
DR HSSP; P02679; 1PZF.
DR MGD; MGI:95526; Fgg.
DR InterPro; IPR002181; Fibrinogen C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 436 AA; 49391 MW; FF45A34B6C92143E CRC64;

PDB; 1BI3; X-ray; C/F=27-435.
PDB; 1MIJ; X-ray; C/F=27-435.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR002181; Fibrinogen C.
InterPro; IPR008994; Fibrinogen C.
Pfam; PF00147; Fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Signal.
CHAIN.
SEQUENCE 435 AA; 49642 MW; 91D2BC7F86850766 CRC64;

Query Match 50.0%; Score 58; DB 2; Length 435;
Best Local Similarity 71.4%; Pred. No. 0.84;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKSMKIRPF 17
DB 402 WYSMKTTMKIIPF 415
|||||:|||||

RESULT 19
FGL1 HUMAN STANDARD; PRT; 312 AA.
ID FGL1 HUMAN STANDARD; PRT; 312 AA.
AC Q08830; Q96KW6; Q96QW6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen-like protein 1 precursor (Hepatocyte-derived fibrinogen-
related protein 1) (HFREP-1) (Hepassocin) (HP-041).
GN Name=FGL1; Synonyms=HFREP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93290661; PubMed=8390249;
RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
RA Hirohashi S.;
RT "Molecular cloning and initial characterization of a novel fibrinogen-
related gene, HFREP-1."
RL Biochem. Biophys. Res. Commun. 193:681-687 (1993).
RN [2]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21363035; PubMed=11470158; DOI=10.1016/S0167-4781(01)00249-4;
RA Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,
RA Morimoto S., Shikawa K.;
RT "Molecular cloning and functional expression analysis of a cDNA for
human hepsocin, a liver-specific protein with hepatocyte mitogenic
activity."
RL Biochim. Biophys. Acta 1520:45-53 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver, and Salivary gland;
RX Submitted (DSC-2001) to the ENBL/GenBank/DBJ databases.
RL EMBL; BC019506; AAH19506.1; -.
DR EMBL; BC019828; AAH19828.1; -.
DR HSSP; P02679; 1PZF.
DR MGD; MGI:95526; Fgg.
DR InterPro; IPR002181; Fibrinogen C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 436 AA; 49391 MW; FF45A34B6C92143E CRC64;

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CC EMBL; D14446; BAA03336.1; -;
CC EMBL; D87342; BAB70690.1; -;
CC EMBL; BC007047; AA07047.1; -;
CC PIR; JN0596; JN0596.
CC HSSP; P02671; 1PZD.
CC Genew; HGNC:3695; FGL1.
CC MIM; 605776; -;
CC GO; GO:0005577; C:fibrinogen complex; TAS.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; Fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Direct protein sequencing; Signal.
FT SIGNAL 1 22
FT CHAIN 23 312 Fibrinogen-like protein 1.
FT DOMAIN 78 305 Fibrinogen C-terminal.
FT DISULFID 26 26 Interchain (Potential).
FT DISULFID 83 112 By similarity.
FT DISULFID 248 261 By similarity.
FT CONFLICT 15 15 I -> T (in Ref. 3).
FT CONFLICT 69 69 N -> D (in Ref. 1).
FT CONFLICT 72 72 I -> V (in Ref. 1).
FT CONFLICT 105 105 P -> L (in Ref. 2).
SQ SEQUENCE 312 AA; 36391 MW; 26BC82124E8660C2 CRC64;

Query Match 48.3%; Score 56; DB 1; Length 312;
Best Local Similarity 55.0%; Pred. No. 1.2;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | | : | | | | |
Db 290 GWMYSLKSVVMKIRPNDPFI 309

RESULT 20
Q8NG32 Q8NG32 PRELIMINARY; PRT; 312 AA.
AC Q8NG32;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LFIRE1.
GN Name=LFIRE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Yan J., Yu Y., Wang N., Xu Y.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF168954; AAM88911.1; -;
DR HSSP; P02671; 1PZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 312 AA; 36377 MW; 7330F3D55A0BD619 CRC64;

Query Match 48.3%; Score 56; DB 2; Length 312;
Best Local Similarity 55.0%; Pred. No. 1.2;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKMSMKIRP--FFP 19

Db 290 GWMYSLKSVVMKIRPNDPFI 309
| | | | | : | | | | |

RESULT 21
AAP35281 AAP35281 PRELIMINARY; PRT; 312 AA.
AC AAP35281;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibrinogen-like 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSS in BD Creator(TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RE EMBL; BT006635; AAP35281.1; -;
SQ SEQUENCE 312 AA; 36379 MW; 9297153AEA746C31 CRC64;

Query Match 48.3%; Score 56; DB 2; Length 312;
Best Local Similarity 55.0%; Pred. No. 1.2;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | | : | | | | |
Db 290 GWMYSLKSVVMKIRPNDPFI 309

RESULT 22
Q71KU9 Q71KU9 PRELIMINARY; PRT; 314 AA.
AC Q71KU9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MFIRE1.
GN Name=MFIRE1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Yan J., Ying H., Gu F., He J., Li Y., Liu H., Xu Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; AP478470; AAO05798.1; -;
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 314 AA; 36438 MW; 61795498265E76B2 CRC64;

Query Match 48.3%; Score 56; DB 2; Length 314;
Best Local Similarity 55.0%; Pred. No. 1.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | | : | | | | |
Db 292 GWMYSLKSVVMKIRPNDPFI 311

RESULT 23
Q8VC25 Q8VC25 PRELIMINARY; PRT; 314 AA.
ID Q8VC25


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AC Q8VC25;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Fibrinogen-like protein 1.
GN Name=Fgll;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
RA Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
PL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; BC021946; AA021946.1; -.
DR HSP; P02671; IFLD.
DR MGP; MG1:102795; Fgll.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 314 AA; 36439 MW; 52C16CA9C2D0386A CRC64;

Query Match 48.3%; Score 56; DB 2; Length 314;
Best Local Similarity 55.0%; Pred. No. 1.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GSWYSMRKMSKIRP--FFP 19
Db 292 GWYSLKSVVMKIRPSDFIP 311
| | | | | : | | | | |
| | | | | : | | | | |

RESULT 24
AAQ05798 PRELIMINARY; PRT; 314 AA.
ID AAQ05798;
AC AAQ05798;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE MFIRE1.
GN MFIRE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
RA Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
PL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; BC021946; AA021946.1; -.
DR HSP; P02671; IFLD.
DR MGP; MG1:102795; Fgll.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 314 AA; 36439 MW; 52C16CA9C2D0386A CRC64;

Query Match 48.3%; Score 56; DB 2; Length 314;
Best Local Similarity 55.0%; Pred. No. 1.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GSWYSMRKMSKIRP--FFP 19
Db 292 GWYSLKSVVMKIRPSDFIP 311
| | | | | : | | | | |
| | | | | : | | | | |

RESULT 25
FIBG BOVIN STANDARD; PRT; 444 AA.
ID FIBG_BOVIN STANDARD; PRT; 444 AA.
AC P12739;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen gamma-B chain precursor (Gamma').
GN Name=FGG;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89366676; PubMed=2771651;
RA Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
RT "Nucleotide and deduced amino acid sequence of a gamma subunit of
RT bovine fibrinogen."
RL Nucleic Acids Res. 17:6397-6397 (1989).
RN [2]
RP SEQUENCE OF 25-63.
RX MEDLINE=77112616; PubMed=836881;
RA Timpl R., Fietzek P.P., Wachter E., van Delden V.;
RT "Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. II.
RT Isolation and sequence analysis of the chain constituents from the
RT amino terminal region."
RL Biochim. Biophys. Acta 490:420-429 (1977).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot. The soft clot is converted
CC into the hard clot by factor XIIIa which catalyzes the epsilon-
CC (gamma-glutamyl)lysine cross-linking between gamma chains
CC (stronger) and between alpha chains (weaker) of different
CC monomers.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; X15556; CAA33562.1; -.
CC PIR; A05295; A05295.
CC PIR; S05313; S05313.
CC PDB; 1DEQ; X-ray; C/F=25-436.

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DR PDB; 1JY2; X-ray; P/S=25-72.
DR PDB; 1JY3; X-ray; P/S=25-72.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW 3D-structure; Blood coagulation; Calcium; Direct protein sequencing;
KW Glycoprotein; Plasma; Platelet; Signal.
FT SIGNAL 1 24
FT CHAIN 25 444 Fibrinogen gamma-B chain.
FT CARBOHYD 76 76 N-linked (GlcNAc... ) (Probable).
FT DISULFID 177 205 By similarity.
FT DISULFID 351 364 By similarity.
FT DISULFID 32 32 Interchain (with C-33).
FT DISULFID 33 33 Interchain (with C-32).
FT DISULFID 43 43 Interchain (with alpha).
FT DISULFID 47 47 Interchain (with beta).
FT DISULFID 159 159 Interchain (with alpha).
FT DISULFID 163 163 Interchain (with alpha).
FT TURN 29 31
FT TURN 33 34
FT HELIX 37 39
FT STRAND 42 44
FT HELIX 46 71
SQ SEQUENCE 444 AA; 50244 MW; 4573C994DE715C49 CRC64;

Query Match 48.3%; Score 56; DB 1; Length 444;
Best Local Similarity 62.5%; Pred. No. 1.8;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKQSMKIRP 16
DB 398 KSRWYSMKETTKIIP 413

RESULT 26
FIBG RAT
ID_FIBG RAT STANDARD; PRT; 445 AA.
AC P02680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen gamma chain precursor.
GN Name:Fbg;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129318; PubMed=6897622;
RA Crabtree G.R., Kant J.A.;
RT "Organization of the rat gamma-fibrinogen gene: alternative mRNA
RT splice patterns produce the gamma A and gamma B (gamma ') chains of
RT fibrinogen.";
RL Cell 31:159-166(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87174801; PubMed=3562236;
RA Morgan J.G., Holbrook N.J., Crabtree G.R.;
RT "Nucleotide sequence of the gamma chain gene of rat fibrinogen:
RT conserved intronic sequences";
RL Nucleic Acids Res. 15:2774-2776 (1987).
RN [3]
RP SEQUENCE OF 1-102 FROM N.A.
RX MEDLINE=84194000; PubMed=6232608;
RA Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
RT "Potential basis for regulation of the coordinately expressed
RT fibrinogen genes: homology in the 5' flanking regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.

```

```

CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Gamma-B;
CC IsoId=P02680-1; Sequence=Displayed;
CC Name=Gamma-A;
CC IsoId=P02680-2; Sequence=VSP_001538, VSP_001539;
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot. The soft clot is converted
CC into the hard clot by factor XIIIa which catalyzes the epsilon-
CC (gamma-glutamyl)lysine cross-linking between gamma chains
CC (stronger) and between alpha chains (weaker) of different
CC monomers.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00733; -; NOT ANNOTATED_CDS.
CC EMBL; J00734; -; NOT ANNOTATED_CDS.
CC EMBL; J00735; -; NOT ANNOTATED_CDS.
CC EMBL; X05860; CAA29289.1; -.
CC EMBL; X05861; CAA29289.1; JOINED.
CC EMBL; K01337; AAA98626.1; -.
CC PIR; A90828; FGRTGA.
CC HSSP; P02679; 1FID.
CC RGD; 2613; Fgg.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; Fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Alternative splicing; Blood coagulation; Calcium; Glycoprotein;
KW Plasma; Platelet; Signal.
FT SIGNAL 1 25
FT CHAIN 26 445 Fibrinogen gamma chain.
FT DISULFID 34 34 Interchain (with gamma chain) (By
FT similarity).
FT DISULFID 35 35 Interchain (with gamma chain) (By
FT similarity).
FT DISULFID 45 45 Interchain (with beta chain) (By
FT similarity).
FT DISULFID 49 49 Interchain (with alpha chain) (By
FT similarity).
FT DISULFID 161 161 Interchain (with beta chain) (By
FT similarity).
FT DISULFID 165 165 Interchain (with gamma chain) (By
FT similarity).
FT DISULFID 179 208 By similarity.
FT DISULFID 352 365 By similarity.
FT VARSEPLIC 435 437 SVE -> GDM (in isoform Gamma-A).
FT /FTId=VSP_001538.
FT VARSPPLIC 438 445 Missing (in isoform Gamma-A).
FT /FTId=VSP_001539.
FT CONFLICT 296 296 E -> G (in cDNA).
FT SEQUENCE 445 AA; 50632 MW; 9D61CCC0168B17A9 CRC64;
SQ

Query Match 48.3%; Score 56; DB 1; Length 445;
Best Local Similarity 58.8%; Pred. No. 1.8;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKQSMKIRP 17
DB 399 KTRWYSMKETTKIIP 415

```

RESULT 27
 O43827 PRELIMINARY; PRT; 346 AA.
 AC O43827;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CD76 (Angiopoietin-like factor) (NL4).
 GN Name=CD76; ORFNames=UNQ313;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cornea;
 RX MEDLINE=98394383; PubMed=9727400;
 RA Peak R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
 RT "Molecular cloning of a new angiopoietin-like factor from the human
 RT cornea.";
 RL Invest. Ophthalmol. Vis. Sci. 39:1782-1788(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21318995; PubMed=11426320;
 RA Stover C., Endo Y., Takahashi M., Lynch N., Constantinescu C.,
 RA Vorup-Jensen T., Thiel S., Friedl H., Hankeln T., Hall R., Gregory S.,
 RA Fujita T., Schwaebler W.;
 RT "The human gene for mannan-binding lectin-associated serine protease-2
 RT (MASP-2), the effector component of the lectin route of complement
 RT activation, is part of a tightly linked gene cluster on chromosome
 RT 1p36.2-3.";
 RL Genes Immun. 2:119-127(2001).
 [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Skin;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richard S., Worley K.C., Hake S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Mair M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Skin;
 RC Straubeberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 [5]
 RN SEQUENCE FROM N.A.
 RP Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22887296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yaneura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; Y16132; CAA76078.1; -;
 DR EMBL; AJ300188; CAC15571.1; -;
 DR EMBL; BC001881; AAH01881.1; -;
 DR EMBL; BT009802; AAP88804.1; -;
 DR EMBL; AY358301; AAQ88668.1; -;
 DR HSP; Q908W6; IUC9.
 DR GO; GO:0006979; P:response to oxidative stress; TAS.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;
 Query Match 44.8%; Score 52; DB 2; Length 346;
 Best Local Similarity 60.0%; Pred. No. 6.3;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 GSWYSMRKMSMKIRP 16
 Db 327 GSTYSLKRVEMKIRP 341
 |||:|||||
 |||:|||||
 RESULT 28
 AAQ88668 PRELIMINARY; PRT; 346 AA.
 AC AAQ88668;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE NL4.
 GN UNQ313.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yaneura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 RT Bioinformatics Assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY358301; AAQ88668.1; -;
 SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;
 Query Match 44.8%; Score 52; DB 2; Length 346;
 Best Local Similarity 60.0%; Pred. No. 6.3;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 GSWYSMRKMSMKIRP 16
 Db 327 GSTYSLKRVEMKIRP 341
 |||:|||||
 |||:|||||
 RESULT 29
 Q28763

RT subunit: a novel exon conferring marked homology to beta and gamma
RT subunits.";
RL Biochemistry 31:11968-11972(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RA Chung D.W., Grieninger G.;
RT "Fibrinogen DNA and protein sequences.";
RL (In) Ebert R.F. (eds.);
RL Index of variant human fibrinogens, pp.13-24, CRC Press, Boca Raton
RL (1994).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
RP ALA-456.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNP. NHLBI HL6682 program for genomic applications, UW-
RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-655 FROM N.A. (ISOFORM ALPHA-E).
RC TISSUE=Liver;
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=83247396; PubMed=6575389;
RA Kant J.A., Lord S.T., Crabtree G.R.;
RT "Partial mRNA sequences for human A alpha, B beta, and gamma
RT fibrinogen chains: evolutionary and functional implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
RN [6]
RP SEQUENCE OF 1-629 FROM N.A.
RX MEDLINE=8228432; PubMed=6688355;
RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the alpha chain of human fibrinogen.";
RL Biochemistry 22:3237-3244(1983).
RN [7]
RP SEQUENCE OF 20-629.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT structural variants.";
RL (In) Peeters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL Pergamon Press, Oxford (1980).
RN [8]
RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
RX MEDLINE=80088231; PubMed=518846;
RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Overlapping sequences providing the complete sequence.";
RL Biochemistry 18:5410-5416(1979).
RN [9]
RP SEQUENCE OF 110-156 FROM N.A.
RX MEDLINE=8406977; PubMed=6689067;
RA Imam A.M., Eaton M.A., Williamson R., Humphries S.;
RT "Isolation and characterization of cDNA clones for the A alpha- and
RT gamma-chains of human fibrinogen.";
RL Nucleic Acids Res. 11:7427-7434(1983).
RN [10]
RP SEQUENCE OF 605-644 FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=83254384; PubMed=6575700;
RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
RT "Cloning of fibrinogen genes and their cDNA.";
RL Ann. N. Y. Acad. Sci. 408:449-456(1983).
RN [11]
RP SEQUENCE OF 20-35.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).

RN [12]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=80088230; PubMed=518845;
RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Exact location of cross-linking acceptor sites.";
RL Biochemistry 18:5405-5410(1979).
RN [13]
RP CROSS-LINKING ACCEPTOR SITES
RX MEDLINE=78130085; PubMed=632262;
RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RT "Localization of the alpha-chain cross-link acceptor sites of human
RT fibrin.";
RL J. Biol. Chem. 253:2184-2195(1978).
RN [14]
RP VARIANT, AND DISULFIDE BONDS.
RX MEDLINE=76225080; PubMed=936108;
RA Blomback B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL Thromb. Res. 8:639-658(1976).
RN [15]
RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RT "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
RN [16]
RP CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
RX MEDLINE=87057190; PubMed=2877981;
RA Kimura S., Aoki N.;
RT "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
RL J. Biol. Chem. 261:15591-15595(1986).
RN [17]
RP PHOSPHORYLATION.
RX MEDLINE=84104274; PubMed=6318767;
RA Itarte E., Plana M., Guasch M.D., Martos C.;
RT "Phosphorylation of fibrinogen by casein kinase 1.";
RL Biochem. Biophys. Res. Commun. 117:631-636(1983).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
RX MEDLINE=92218459; PubMed=1560020;
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT "The structure of residues 7-16 of the A alpha-chain of human
RT fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.
RX MEDLINE=97472408; PubMed=9333233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
RT crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RT different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
RX MEDLINE=98356117; PubMed=9689040;
RA Spraggon G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian L.,
RA Redman C., Doolittle R.F., Grieninger G.;
RT "Crystal structure of a recombinant alpha2C domain from human
RT fibrinogen-420.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
RN [22]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";

RL Biochemistry 38:2941-2946(1999).
 RN [23]
 RP VARIANT KYOTO-2.
 RX MEDLINE=91300048; PubMed=2070049;
 RA Yoshida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
 RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule
 characterized by the replacement of A alpha proline-18 by leucine.";
 RL Blood 78:149-153(1991).
 RN [24]
 RN VARIANT LIMA.
 RP MEDLINE=92340680; PubMed=1634621;
 RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
 RA Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H.,
 RA Perez-Requejo J.L., Matsuda M.;
 RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A alpha-arginine-
 RT 141 to serine substitution associated with extra N-glycosylation at A
 RT alpha-asparagine-139. Impaired fibrin gel formation but normal fibrin-
 RT facilitated plasminogen activation catalyzed by tissue-type
 RT plasminogen activator.";
 RT J. Clin. Invest. 90:67-76(1992).
 RN [25]
 RN VARIANT CARACAS-2.
 RP MEDLINE=91268018; PubMed=1675636;
 RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
 RA Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
 RA Arocha-Pinango C.L., Matsuda M.;
 RT "An A alpha Ser-434 to N-glycosylated Asn substitution in a
 RT dysfibrinogen, fibrinogen Caracas II, characterized by impaired fibrin
 RT gel formation.";
 RT J. Biol. Chem. 266:11575-11581(1991).
 RN [26]
 RP VARIANT DUSART.
 RX MEDLINE=93232289; PubMed=8473507;
 RA Koopman J., Haverkate F., Grimbergen J., Lord S.T., Moessons M.W.,
 RA Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
 RA Caen J.P.;
 RT "Molecular basis for fibrinogen Duseart (A alpha 554 Arg-->Cys) and its
 RT

Query Match 44.0%; Score 51; DB 1; Length 866;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFPPQ 20
 Db 847 RGADYSLRVRMKIRPLVTQ 866

RESULT 32
 Q8NL80 Q8NL80 PRELIMINARY; PRT; 1643 AA.
 AC Q8NL80;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Restriction enzymes type I helicase subunits and related
 DE helicases.
 GN OrderedLocNames=Cgl3069;
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa S.;
 RA "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AP005283; BAC00463.1; --.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
 DR GO; GO:0015668; F:type III site-specific deoxyribonuclease ac. . .; IEA.

DR GO; GO:0006306; P:DNA methylation; IEA.
 DR GO; GO:0009307; P:DNA restriction; IEA.
 DR InterPro; IPR006130; Asp/Orn_Cotranf.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase C.
 DR InterPro; IPR002296; N12N6_mtfrase.
 DR InterPro; IPR002052; N6_Mtase.
 DR InterPro; IPR006935; ResIII.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF04851; ResIII; 1.
 DR PRINTS; PR00507; N12N6MTFRASE.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; UNKNOWN_1.
 DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
 KW Complete proteome; Helicase.
 SQ SEQUENCE 1643 AA; 183351 MW; 6AA4C2121894CDE1 CRC64;
 Query Match 44.0%; Score 51; DB 2; Length 1643;
 Best Local Similarity 37.8%; Pred. No. 48;
 Matches 14; Conservative 1; Mismatches 6; Indels 16; Gaps 1;

QY 1 KGSWYSMRKMSK-----IRPFPPQ 21
 Db 1297 KISWDSNLKMSLSRGDTFSPDPSSIQMSLYRPFPPQ 1333

RESULT 33
 Q6M1E9 Q6M1E9 PRELIMINARY; PRT; 1646 AA.
 AC Q6M1E9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE DNA or RNA helicase of superfamily II.
 GN OrderedLocNames=cg3398;
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RX PubMed=12948626;
 RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
 RA Burkowski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
 RA Goemann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
 RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Pühler A.,
 RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
 RA Tauch A.;
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
 RT and its impact on the production of L-aspartate-derived amino acids
 RT and vitamins.";
 RL J. Biotechnol. 104:5-25(2003).
 DR EMBL; BX921757; CAF19007.1; --.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR InterPro; IPR006130; Asp/Orn_Cotranf.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001650; Helicase C.
 DR InterPro; IPR002296; N12N6_mtfrase.
 DR InterPro; IPR002052; N6_Mtase.
 DR InterPro; IPR006935; ResIII.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR PRINTS; PR00507; N12N6MTFRASE.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; UNKNOWN_1.
 DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
 KW ATP-binding; Helicase; Hydrolase.
 SQ SEQUENCE 1646 AA; 183715 MW; EF060CD1B56248FF CRC64;

Query Match 44.0%; Score 51; DB 2; Length 1646;
 Best Local Similarity 37.8%; Pred. No. 49;
 Matches 14; Conservative 1; Mismatches 6; Indels 16; Gaps 1;

QY 1 KGSWYSMRKMSMK-----IRPFPPQ 21
 DB 1300 KISWDSNLSRGTSPDPSSIQMSLYRPFPPQ 1336

RESULT 34

CAFI9007 PRELIMINARY; PRT; 1646 AA.
 AC CAF19007;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE DNA or RNA helicase of superfamily II.
 GN CG3398.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RX PubMed=12948626;
 RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
 RA Burkowski A., Dusch N., Egeling L., Eikmanns B.J., Gaigalat L.,
 RA Gosemann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
 RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puhler A.,
 RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
 RA Tauch A.;
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
 RT and its impact on the production of L-aspartate-derived amino acids
 RT and vitamins.";
 RL J. Biotechnol. 104:5-25(2003).
 DR EMBL; BX927157; CAF19007.1; -.
 KW Helicase.
 SQ SEQUENCE 1646 AA; 183715 MW; EF060CD1B56248FF CRC64;

Query Match 44.0%; Score 51; DB 2; Length 1646;
 Best Local Similarity 37.8%; Pred. No. 49;
 Matches 14; Conservative 1; Mismatches 6; Indels 16; Gaps 1;

QY 1 KGSWYSMRKMSMK-----IRPFPPQ 21
 DB 1300 KISWDSNLSRGTSPDPSSIQMSLYRPFPPQ 1336

RESULT 35

Q7S213 PRELIMINARY; PRT; 439 AA.
 ID Q7S213
 AC Q7S213;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Fg-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan T., Moore T., Max S.I., Wang J., Helel F.,
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Klein S., Strausberg R.,
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC054185; AAH54185.1; -.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
 SQ SEQUENCE 439 AA; 50046 MW; 6487BDFB3CA9F84 CRC64;

Query Match 43.1%; Score 50; DB 2; Length 439;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRP 16
 DB 398 RSRWYSMKSVTKIIP 413

RESULT 36

Q7TQ70 PRELIMINARY; PRT; 782 AA.
 ID Q7TQ70
 AC Q7TQ70;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Acl873.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
 RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
 RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY310161; AAP78769.1; -.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
 SQ SEQUENCE 782 AA; 86656 MW; 338BC86F2D81DA18 CRC64;

Query Match 43.1%; Score 50; DB 2; Length 782;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 KGSWYSMRKSMKIRPFPPQ 20
Db 763 RGADYSLRAVRMKIRPLVGQ 782

RESULT 37
ID Q8VWV9 PRELIMINARY; PRT; 910 AA.
AC Q8VWV9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative alpha-xylosidase.
GN Name=XYLI;
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Etisolated hypocotyls;
RX MEDLINE=22497948; PubMed=12610215;
RA Sanchez M., Gianzo C., Sampedro J., Revilla G., Zarza I.;
RT "Changes in alpha-xylosidase during Intact and Auxin-Induced Growth of
RT Pine Hypocotyls.;"
RL Plant Cell Physiol. 44:132-138 (2003).
DR EMBL; AF448201; AAL40352.1; -.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000322; Glyco_hydro_31.
DR Pfam; PF01055; Glyco_hydro_31; 1.
DR PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
DR PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.
SQ SEQUENCE 910 AA; 100609 MW; C4B75C7306CC16F9 CRC64;

Query Match 43.1%; Score 50; DB 2; Length 910;
Best Local Similarity 46.7%; Pred. No. 37;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKSMKIR 15
Db 712 KGSWYNLNDMTMAVK 726

RESULT 38
Q901F9
ID Q901F9 PRELIMINARY; PRT; 145 AA.
AC Q901F9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21828184; PubMed=11839150;
RY Yu X.-F., Liu W., Chen J., Kong W., Liu B., Zhu Q., Liang F.,
RA McCutchan F., Piyasirisilp S., Lai S.;
RT "Maintaining low HIV type 1 env genetic diversity among injection drug
RT users infected with a B/C recombinant and CRF01_AE HIV type 1 in
RT southern China.;"
RL AIDS Res. Hum. Retroviruses 18:167-170 (2002).
DR EMBL; AY049934; AAL14374.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
```

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FT NON_TER 1 1
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16048 MW; 6ABB7C2A8EF3D5A0 CRC64;

Query Match 42.7%; Score 49.5; DB 2; Length 145;
Best Local Similarity 40.9%; Pred. No. 6.3;
Matches 9; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

Qy 1 KGSWY-SMRKSMKIRPFPPQ 21
Db 61 KGDWYETLQKVSCKLAHFENK 82

RESULT 39
Q91ZP1
ID Q91ZP1 PRELIMINARY; PRT; 236 AA.
AC Q91ZP1;
DT 01-DRC-2001 (TrEMBLrel. 19, Created)
DT 01-DRC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibrinogen B-beta-chain (Fragment).
GN Name=Fgb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Murakawa M., Freeman M.W.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413205; AAL02225.1; -.
DR MGD; MGI:99501; Fgb.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
FT NON_TER 1 1
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27054 MW; A844F0B40CCB8B01 CRC64;

Query Match 42.2%; Score 49; DB 2; Length 236;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGSWYSMRK 9
Db 228 KGSWYSMR 236

RESULT 40
Q7ZXL3
ID Q7ZXL3 PRELIMINARY; PRT; 343 AA.
AC Q7ZXL3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MG53392 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
```


RA Lyngsoe C., Bouteiller G., Damgaard C.K., Ryom D., Sanchez-Munoz S.,
 RA Norby P.L., Bonven B.J., Joergensen P.;
 RT "Interaction between the transcription factor SPBP and the positive
 RT cofactor RN4. An interplay between protein binding zinc fingers.";
 RL J. Biol. Chem. 275:26144-26149(2000).
 CC -|- FUNCTION: Transcriptional activator that binds to the regulatory
 CC region of MMP3 and thereby controls stromelysin expression. It
 CC stimulates the activity of various transcriptional activators such
 CC as JUN, SP1, PAX6 and ETS1, suggesting a function as a
 CC coactivator.
 CC -|- SUBUNIT: Homodimer (Probable). Interacts with RN4 and JUN. Binds
 CC to the regulatory region of MMP3.
 CC -|- SUBCELLULAR LOCATION: Nuclear.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9EPQ8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9EPQ8-2; Sequence=VSP_003986;
 CC TISSUE SPECIFICITY: Expressed in brain, lung, liver, kidney and
 CC testes.
 CC -|- DEVELOPMENTAL STAGE: Isoform 2 is exclusively expressed at 7-11
 CC days of development. Isoform 1 is found only at low levels in 15-
 CC 17 days embryos.
 CC -|- DOMAIN: The atypical PHD domain functions as a negative modulator
 CC of cofactor binding.
 CC -|- SIMILARITY: Contains 1 A.T hook DNA-binding repeat.
 CC -|- SIMILARITY: Contains 1 PHD-type zinc finger.
 CC -|- CAUTION: Ref.2 sequence differs from that shown due to
 CC frameshifts.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AY007594; AAC28929.1; -;
 CC EMBL; U02822; AA86495.1; ALT_SEQ.
 CC MGD; MG1:108399; Tcf20.
 CC GO; GO:0005634; C:nucleus; ISS.
 CC GO; GO:0003677; F:DNA binding; ISS.
 CC GO; GO:0003713; F:transcription coactivator activity; ISS.
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
 CC InterPro; IPR001965; Znf_PHD.
 CC SMART; SM00249; PHD; 1.
 CC KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
 KW Transcription regulation; Zinc-finger.
 FT DOMAIN 1198 1219 Leucine-zipper.
 FT DOMAIN 1282 1295 Nuclear localization signal.
 FT DNA BIND 1565 1579 A.T hook.
 FT DOMAIN 1604 1628 Nuclear localization signal.
 FT DOMAIN 1812 1819 Nuclear localization signal.
 FT ZN FING 1911 1962 PHD-type (atypical).
 FT DOMAIN 62 69 Poly-Ala.
 FT DOMAIN 173 195 Poly-Gln.
 FT DOMAIN 249 277 Ser-rich.
 FT DOMAIN 322 350 Poly-Gln.
 FT DOMAIN 1585 1592 Poly-Pro.
 FT DOMAIN 1681 1684 Poly-Glu.
 FT DOMAIN 1793 1797 Poly-Glu.
 FT VARSPLIC 1961 1983 CPLEPLQNKTKAGSLSTQSERG -> VRLWR (in
 FT isoform 2).
 FT /FTid=VSP_003986.
 FT A->T: Loss of interaction with RN4; when
 FT associated with S-1702, R-1736 and V-
 FT 1737.
 FT P->S: Loss of interaction with RN4; when
 FT associated with T-1629, R-1736 and V-
 FT 1737.
 FT CG->RV: Loss of interaction with RN4;
 FT 1737

FT MUTAGEN 1926 1926 when associated with T-1629 and S-1702.
 FT C->A: Reduces the inhibitory effect of
 FT the atypical PHD domain.
 FT MUTAGEN 1931 1931 C->A: Reduces the inhibitory effect of
 FT the atypical PHD domain.
 FT MUTAGEN 1936 1936 H->L: Reduces the inhibitory effect of
 FT the atypical PHD domain.
 FT MUTAGEN 1939 1939 C->A: Reduces the inhibitory effect of
 FT the atypical PHD domain.
 SQ SEQUENCE 1983 AA; 215284 MW; E749A9355CB2971B CRC64;
 Query Match 42.2%; Score 49; DB 1; Length 1983;
 Best Local Similarity 47.4%; Pred. No. 1.3e+02;
 Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 Qy 2 GSWYSYRKMSKMKIRPFPPQ 20
 Db 1737 GKWASYRNMGDLFGPFYPQ 1755
 RESULT 44
 ID Q6GLL5 PRELIMINARY; PRT; 313 AA.
 AC Q6GLL5;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22398257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Shac N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marz M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Klein S., Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC074461; AAH74461.1; -;
 DR InterPro; IPR002181; Fibrinogen_C.

DR Pfam: PF00147; Fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 313 AA; 36214 MW; 4B82C05FE7E14451 CRC64;

Query Match 41.4%; Score 48; DB 2; Length 313;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSWYSMRKSMKIR 15
 ID RNP4_METJA STANDARD; PRT; 128 AA.
 AC Q58372;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ribonuclease P protein component 4 (EC 3.1.26.5) (RNase P component 4).
 DE 4).
 GN Names=rnp4; OrderedLocusNames=MJ0962;
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Sutt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Part of ribonuclease P, a protein complex that generates mature tRNA molecules by cleaving their 5' ends (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-extra-nucleotide from tRNA precursor.
 CC -1- SUBUNIT: Consists of a catalytic RNA component and at least 4 protein subunits (Potential).
 CC -1- SIMILARITY: Belongs to the eukaryotic/archaeal RNase P protein component 4 family.

RESULT 45

Q6DJ9 PRELIMINARY; PRT; 343 AA.
 AC Q6DJ9;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RA Klein S., Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 KW EMBL: BC075230; AAH75230.1; .
 KW Hypothetical protein.
 SQ SEQUENCE 343 AA; 39286 MW; DAC9C39F76F13C84 CRC64;

Query Match 41.4%; Score 48; DB 2; Length 343;
 Best Local Similarity 53.3%; Pred. No. 28;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSWYSMRKSMKIRP 16
 ID RNP4_METJA STANDARD; PRT; 128 AA.
 AC Q58372;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ribonuclease P protein component 4 (EC 3.1.26.5) (RNase P component 4).
 DE 4).
 GN Names=rnp4; OrderedLocusNames=MJ0962;
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Sutt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Part of ribonuclease P, a protein complex that generates mature tRNA molecules by cleaving their 5' ends (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-extra-nucleotide from tRNA precursor.
 CC -1- SUBUNIT: Consists of a catalytic RNA component and at least 4 protein subunits (Potential).
 CC -1- SIMILARITY: Belongs to the eukaryotic/archaeal RNase P protein component 4 family.

RESULT 46

RNP4_METJA STANDARD; PRT; 128 AA.
 AC Q58372;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ribonuclease P protein component 4 (EC 3.1.26.5) (RNase P component 4).
 DE 4).
 GN Names=rnp4; OrderedLocusNames=MJ0962;
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Sutt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Part of ribonuclease P, a protein complex that generates mature tRNA molecules by cleaving their 5' ends (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-extra-nucleotide from tRNA precursor.
 CC -1- SUBUNIT: Consists of a catalytic RNA component and at least 4 protein subunits (Potential).
 CC -1- SIMILARITY: Belongs to the eukaryotic/archaeal RNase P protein component 4 family.

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EMBL: U67539; AAB98964.1; .
 PIR: B64420; B64420.
 TIGR: MJ0962;
 HAMAP: MF-00757; 1.
 InterPro: IPR007175; Rpr2.
 Pfam: PF04032; Rpr2; 1.
 Complete proteome; Hydrolase; tRNA processing.
 SQ SEQUENCE 128 AA; 15567 MW; 462D677CE5B159D3 CRC64;

Query Match 40.9%; Score 47.5; DB 1; Length 128;
 Best Local Similarity 35.7%; Pred. No. 12;
 Matches 10; Conservative 7; Mismatches 4; Indels 7; Gaps 1;
 QY 1 KGSW-----YSMRKSMKIRPFPPQ 21
 ID RNP4_METJA STANDARD; PRT; 128 AA.
 AC Q58372;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ribonuclease P protein component 4 (EC 3.1.26.5) (RNase P component 4).
 DE 4).
 GN Names=rnp4; OrderedLocusNames=MJ0962;
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Sutt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Part of ribonuclease P, a protein complex that generates mature tRNA molecules by cleaving their 5' ends (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-extra-nucleotide from tRNA precursor.
 CC -1- SUBUNIT: Consists of a catalytic RNA component and at least 4 protein subunits (Potential).
 CC -1- SIMILARITY: Belongs to the eukaryotic/archaeal RNase P protein component 4 family.

EMBL: U67539; AAB98964.1; .
 PIR: B64420; B64420.
 TIGR: MJ0962;
 HAMAP: MF-00757; 1.
 InterPro: IPR007175; Rpr2.
 Pfam: PF04032; Rpr2; 1.
 Complete proteome; Hydrolase; tRNA processing.
 SQ SEQUENCE 128 AA; 15567 MW; 462D677CE5B159D3 CRC64;

Query Match 40.9%; Score 47.5; DB 1; Length 128;
 Best Local Similarity 35.7%; Pred. No. 12;
 Matches 10; Conservative 7; Mismatches 4; Indels 7; Gaps 1;
 QY 1 KGSW-----YSMRKSMKIRPFPPQ 21
 ID RNP4_METJA STANDARD; PRT; 128 AA.
 AC Q58372;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ribonuclease P protein component 4 (EC 3.1.26.5) (RNase P component 4).
 DE 4).
 GN Names=rnp4; OrderedLocusNames=MJ0962;
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Sutt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Part of ribonuclease P, a protein complex that generates mature tRNA molecules by cleaving their 5' ends (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-extra-nucleotide from tRNA precursor.
 CC -1- SUBUNIT: Consists of a catalytic RNA component and at least 4 protein subunits (Potential).
 CC -1- SIMILARITY: Belongs to the eukaryotic/archaeal RNase P protein component 4 family.

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EMBL: U67539; AAB98964.1; .
 PIR: B64420; B64420.
 TIGR: MJ0962;
 HAMAP: MF-00757; 1.
 InterPro: IPR007175; Rpr2.
 Pfam: PF04032; Rpr2; 1.
 Complete proteome; Hydrolase; tRNA processing.
 SQ SEQUENCE 128 AA; 15567 MW; 462D677CE5B159D3 CRC64;

Query Match 40.9%; Score 47.5; DB 1; Length 128;
 Best Local Similarity 35.7%; Pred. No. 12;
 Matches 10; Conservative 7; Mismatches 4; Indels 7; Gaps 1;
 QY 1 KGSW-----YSMRKSMKIRPFPPQ 21
 ID RNP4_METJA STANDARD; PRT; 128 AA.
 AC Q58372;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ribonuclease P protein component 4 (EC 3.1.26.5) (RNase P component 4).
 DE 4).
 GN Names=rnp4; OrderedLocusNames=MJ0962;
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Sutt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Part of ribonuclease P, a protein complex that generates mature tRNA molecules by cleaving their 5' ends (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-extra-nucleotide from tRNA precursor.
 CC -1- SUBUNIT: Consists of a catalytic RNA component and at least 4 protein subunits (Potential).
 CC -1- SIMILARITY: Belongs to the eukaryotic/archaeal RNase P protein component 4 family.

```
AC O59042;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PH1324.
GN OrderedLocustName=PH1324.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OC NCBI_TaxID=53953;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=OT3;
RC MEDLINE=98344137; PubMed=9679194;
RA Kavarabavasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kousugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000006; BAA30430.1; -.
DR FIRM; F71003.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 125 AA; 13657 MW; C6613D9E8D711154 CRC64;

Query Match 40.5%; Score 47; DB 2; Length 125;
Best Local Similarity 42.1%; Pred. No. 14;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 3 SWYSMRKMSKIRPFFPQ 21
Db 101 SWVSIFITLSVIFPFIQ 119

RESULT 48
Q9HBP3 PRELIMINARY; PRT; 244 AA.
ID Q9HBP3
AC Q9HBP3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218015; AAG17257.1; -.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27825 MW; E9D0ACBF87A7139E CRC64;

Query Match 40.5%; Score 47; DB 2; Length 244;
Best Local Similarity 56.2%; Pred. No. 28;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSKIRP 16
Db 226 KGSYSLKATWMIKP 241
```

```
RESULT 49
Q7PZN3 PRELIMINARY; PRT; 308 AA.
ID Q7PZN3
AC Q7PZN3
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP9446.
GN Name=agCG55756; ORFNames=ENSANGG000000013971;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PEST;
RC Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008986; EAA00222.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
SQ SEQUENCE 308 AA; 35657 MW; 1FB23687EBFB85F8 CRC64;

Query Match 40.5%; Score 47; DB 2; Length 308;
Best Local Similarity 43.8%; Pred. No. 36;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSKIRP 16
Db 291 RGSYSLKSTKMVRP 306

RESULT 50
Q7QNI7 PRELIMINARY; PRT; 310 AA.
ID Q7QNI7
AC Q7QNI7
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP5142.
GN Name=agCG43338; ORFNames=ENSANGG000000011322;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PEST;
RC Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01000889; EAA01903.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
SQ SEQUENCE 310 AA; 35997 MW; 53E335070B722B23 CRC64;

Query Match 40.5%; Score 47; DB 2; Length 310;
Best Local Similarity 43.8%; Pred. No. 36;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSKIRP 16
Db 293 RGSYSLKSTKMVRP 308
```

Search completed: January 18, 2005, 11:08:07
Job time : 196 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 11:04:00 ; Search time 151 Seconds
(without alignments)

49.890 Million cell updates/sec

Title: US-09-487-790A-1

Perfect score: 116

Sequence: 1 KGSWYSMRKMSMKIRPFPPQ 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 65 summaries

Database :

A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	21	3	AA52600 Synthetic
2	116	100.0	21	4	AA65028 Haptotact
3	116	100.0	21	8	ADO85130 Human-der
4	116	100.0	453	4	AAW78493 Human pro
5	116	100.0	489	5	ABU60918 Lung spec
6	116	100.0	491	2	AA82243 Human fib
7	116	100.0	491	4	AAW78492 Human pro
8	116	100.0	491	6	AAE36413 Human FBG
9	116	100.0	491	7	ADP65229 Human fib
10	116	100.0	491	7	ADP65300 Human fib
11	116	100.0	502	4	AAU31380 Novel hum
12	116	100.0	539	4	AAW78491 Human pro
13	113	97.4	488	8	AAE76868 Human pro
14	113	97.4	495	4	AAW79475 Human pro
15	113	97.4	495	4	AAW79476 Human pro
16	113	97.4	495	4	AAW79477 Human pro
17	109	94.0	491	7	ADD69271 Human fib
18	109	94.0	491	7	ADD69272 Human fib
19	106	91.4	479	8	ADI82107 Fibrinoge
20	75	64.7	14	4	AAW97040 Human pep
21	75	64.7	14	4	AAW97039 Human pep
22	75	64.7	14	4	AAW00113 Human ang
23	72	62.1	14	4	AAW00114 Human ang
24	60	51.7	16	4	AA65026 Haptotact
25	60	51.7	16	8	ADO85142 Human-der

26	60	51.7	20	4	AA65016 Human fib
27	60	51.7	20	8	ADO85132 Human-der
28	60	51.7	194	3	AAO39176 Human sec
29	60	51.7	194	3	AAO39177 Human sec
30	60	51.7	437	8	ADK70498 Respirato
31	60	51.7	437	8	ADL61247 Human pro
32	60	51.7	453	2	AA82246 Human fib
33	60	51.7	453	2	AA82245 Human fib
34	60	51.7	453	7	ADD45364 Human pro
35	60	51.7	453	8	ADQ30579 Pancreas
36	60	51.7	454	3	AA84551 Partial h
37	60	51.7	454	3	AA94009 Amino aci
38	58	50.0	20	5	ABG62851 Ligand/re
39	58	50.0	20	8	ADM73982 Ligand/re
40	58	50.0	27	5	ABG62912 Ligand/re
41	58	50.0	27	8	ADM74055 Ligand/re
42	58	50.0	28	1	AA640614 Sequence
43	58	50.0	73	2	AAW57671 Collagen-
44	58	50.0	75	2	AA80332 Protein p
45	58	50.0	75	2	AAW49716 Protein p
46	58	50.0	75	2	AAW49721 Protein p
47	58	50.0	125	2	AA80333 Collagen-
48	58	50.0	198	2	AAW57672 Protein p
49	58	50.0	314	2	AAW49722 Protein p
50	58	50.0	314	2	AAW49722 Protein p
51	57	49.1	10	4	AA65022 Human fib
52	57	49.1	10	8	ADO85138 Human-der
53	57	49.1	411	2	AA84650 Fibrinoge
54	56	48.3	50	4	AAW16157 Peptide #
55	56	48.3	50	4	ABW35142 Peptide #
56	56	48.3	50	4	ABG50006 Human liv
57	56	48.3	282	6	ABR48466 Human Fra
58	56	48.3	312	2	AA65760 Human hep
59	56	48.3	312	2	AA94317 Hepatocyt
60	56	48.3	312	2	AA94316 Hepatocyt
61	56	48.3	312	8	ADL13280 Human ste
62	56	48.3	339	3	AAW43637 Human can
63	56	48.3	437	7	ADD45362 Rat Prote
64	54	46.6	437	7	ADD69273 Human fib
65	54	46.6	453	7	ADD69274 Human fib

ALIGNMENTS

RESULT 1

AA52600

ID AA52600 standard; peptide; 21 AA.

XX AA52600;

DT 07-MAR-2000 (first entry)

XX Synthetic fibrinogen C-terminus peptide, peptide-09.

XX Fibrinogen; C-terminus; cell adhesion; cell binding; proliferation;

XX wound healing; diabetes mellitus; clotting; coagulation; disorder;

XX haemophilia A; factor VIII deficiency; haemophilia B;

XX factor IX deficiency; cell culture; separation; cell transplantation;

XX therapeutic structure; research tool; diagnosis.

XX Synthetic.

XX WO9961041-A1.

XX 02-DEC-1999.

XX 26-MAY-1999; 99WO-US011517.

XX 27-MAY-1998; 98US-00084371.

XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PA (VITE-) VI TECHNOLOGIES INC.

XX
PI Gorodetsky R, Marx G;
XX WPI; 2000-062582/05.
XX
XX New peptides corresponding to fibrinogen carboxy terminus, used for
PT promoting wound healing.
PT
XX Claim 1; Page 6; 46pp; English.
XX
XX This sequence represents a synthetic peptide, peptide-09, which
CC corresponds to a fibrinogen beta chain C-terminal sequence. The invention
CC relates to novel fibrinogen C-terminal peptides, peptide-09 (AA52600),
CC peptide-70 (AA52693) and peptide-71 (AA52694). These claimed peptides
CC have cell adhesive effects, with peptide-09 being the most potent for
CC cell binding, and peptide-71 being the next most potent. Peptide-71 was
CC also found to have cell proliferative effects. The peptides can be used
CC to promote healing of a wound in a patient. They can also be used for
CC diseases characterised by the absence of a cellular product, e.g.,
CC diabetes mellitus type I, haemophilia A (factor VIII deficiency), and
CC haemophilia B (factor IX deficiency). They can also be used for the
CC growth and transport of cells in cell culturing systems, the separation
CC of different types of cells from mixed cell cultures, and the
CC transplantation of cells into tissues or cell cultures. They can be used
CC for producing therapeutic structures, e.g., gels, prosthetic devices or
CC collagen sheets. The peptides can also be used as tools for performing
CC analysis of other physiological systems, and for further research and
CC development, for example, to identify and isolate cell receptors. The
CC peptides can also be used in diagnosis, e.g., of blood coagulation
CC disorders
XX
XX Sequence 21 AA;
SQ

Query Match 100.0%; Score 116; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPFPPQQ 21
Db 1 KGSWYSMRKMSMKIRPFPPQQ 21

RESULT 2
AAG5028
ID AAG65028 standard; peptide; 21 AA.
XX
AC AAG65028;
XX
XX 01-OCT-2001 (first entry)
XX
XX Haptotactic peptide #1.
DE
XX Human; cell attachment peptide; haptotactic; fibrinogen; wound healing;
KW angiotensin; tenascin; microfibril-associated glycoprotein-4; MRAP4;
KW cell separation; cell receptor.
XX
XX Unidentified.
OS
XX WO200153324-A2.
XX
XX 26-JUL-2001.
XX
XX 21-JAN-2001; 2001WO-IL000057.
XX
XX 20-JAN-2000; 2000US-00487790.
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA
XX Marx G, Gorodetsky R;
PI
XX WPI; 2001-457595/49.
XX
XX Novel haptotactic peptides useful for enhancing wound healing and

PT osteogenesis.
XX
XX Disclosure; Page 14; 43pp; English.
XX
XX The present invention provides haptotactic peptides with sequences
CC homologous to sequences found within the C-termini of fibrinogen, and
CC which are characterised by their ability to induce cell attachment to a
CC surface to which the peptide is bound. These are useful in the treatment
CC of wounds and diseases, to separate different types of cells in culture,
CC to analyse cell receptor mechanisms and to design peptide-derivatised
CC drugs. The present sequence is a known haptotactic peptide
XX
XX Sequence 21 AA;
SQ

Query Match 100.0%; Score 116; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPFPPQQ 21
Db 1 KGSWYSMRKMSMKIRPFPPQQ 21

RESULT 3
ADO85130
ID ADO85130 standard; peptide; 21 AA.
XX
AC ADO85130;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human-derived haptotactic peptide SeqID1.
XX
XX haptotactic; liposomal composition; carboxy termini; fibrinogen chain;
KW liposome; lipid bilayer; aqueous compartment; delivery; human.
XX
XX Homo sapiens.
XX
XX WO2004041298-A1.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-IL000911.
XX
XX 03-NOV-2002; 2002IL-00152609.
XX
XX (HAPT-) HAPTO BIOTECH INC.
XX
XX Marx G, Gorodetsky R;
PI
XX WPI; 2004-449501/42.
XX
XX Haptotactic peptide liposomal composition, useful for enhancing liposome
PT uptake into cells, comprising peptide capable of eliciting cell
PT attachment responses and sequence similarity to haptotactic peptides and
PT liposome having lipid bilayers.
XX
XX Claim 3; SEQ ID NO 1; 53pp; English.
XX
XX This invention relates to a novel haptotactic peptide liposomal
CC composition, which comprises at least one type of peptide and one type of
CC liposome, where the peptide elicits cell attachment responses and has an
CC amino acid sequence that is at least 60% homologous to a haptotactic
CC peptide present within the carboxy termini of fibrinogen chains, and the
CC liposome has at least one lipid bilayer enclosing an aqueous compartment.
CC The invention is useful for enhancing liposome uptake into cells or for
CC enhancing intracellular uptake of biologically active compounds by low-
CC permeability through the cell membrane using a haptotactic-peptide
CC liposomal composition. The invention may be particularly useful for
CC enhancing the delivery of pharmaceutical agent into cells, for enhancing
CC the delivery of diagnostic agent into cells or for enhancing delivery of
CC cosmetically effective liposomes into cells, where the liposomes of the
CC composition have a cosmetic beneficial effect. The present sequence is

CC that of a human-derived haptotactic peptide which may be used during the
CC creation of the compositions of the invention.

XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 116; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFPPQQ 21
|||||
Db 1 KGSWYSMRKMSKIRPFPPQQ 21

RESULT 4
AAM78493
ID AAM78493 standard; protein; 453 AA.

XX
AC AAM78493;

XX
DT 06-NOV-2001 (first entry)

XX
DE Human protein SEQ ID NO 1155.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

XX
OS Homo sapiens.

XX
PN WO200157190-A2.

XX
PD 09-AUG-2001.

XX
PF 05-FEB-2001; 2001WO-US004098.

XX
PR 03-FEB-2000; 2000US-00496914.

XX
PR 27-APR-2000; 2000US-00560875.

XX
PR 20-JUN-2000; 2000US-00598075.

XX
PR 19-JUL-2000; 2000US-00620325.

XX
PR 01-SEP-2000; 2000US-00654936.

XX
PR 15-SEP-2000; 2000US-00663561.

XX
PR 20-OCT-2000; 2000US-00693325.

XX
PR 30-NOV-2000; 2000US-00728422.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX
DR WPI; 2001-476283/51.

XX
DR N-PSDB; AAKS1626.

XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.

XX
PS Claim 20; Page 3390-3391; 6221pp; English.

XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

XX
SQ Sequence 453 AA;

Query Match 100.0%; Score 116; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFPPQQ 21
|||||
Db 433 KGSWYSMRKMSKIRPFPPQQ 453

RESULT 5
ABU60918

ID ABU60918 standard; protein; 489 AA.

XX
AC ABU60918;

XX
DT 08-MAY-2003 (first entry)

XX
DE Lung specific protein (LSP) #21.

XX Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal.

XX
OS Homo sapiens.

XX
PN WO200268633-A2.

XX
PD 06-SEP-2002.

XX
PF 21-NOV-2001; 2001WO-US043612.

XX
PR 22-NOV-2000; 2000US-0252500P.

XX
PA (DIAD-) DIADEXUS INC.

XX
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;

XX
DR WPI; 2002-713376/77.

XX
PT New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.

XX
PS Claim 11; Page 320-322; 389pp; English.

XX
CC The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This is the amino
CC acid sequence of a lung specific nucleic acid

XX
SQ Sequence 489 AA;

Query Match 100.0%; Score 116; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFPPQQ 21
|||||
Db 469 KGSWYSMRKMSKIRPFPPQQ 489

RESULT 6
AAR82243

ID AAR82243 standard; protein; 491 AA.
 XX
 AC AAR82243;
 XX
 DT 26-OCT-1996 (first entry)
 XX
 DE Human fibrinogen B-beta chain protein.
 XX
 DE Human fibrinogen B-beta chain; transgenic animal milk; treatment;
 KW sheep beta-lactoglobulin signal peptide fusion protein;
 KW surgical adhesive.
 KW
 XX Homo sapiens.
 OS
 XX W09523868-A1.
 PN
 XX 08-SEP-1995.
 PD
 XX
 XX 01-MAR-1995; 95WO-US002648.
 PF
 XX 03-MAR-1994; 94US-00206176.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA (PHAR-) PHARM PROTEINS LTD.
 PA
 XX Garner I, Dalrymple MA, Prunkard DE, Foster DC;
 PI
 XX WPI; 1995-320582/41.
 DR N-PSDB; AAT03852.
 DR
 XX Production of fibrinogen in transgenic mammals - by introducing DNA
 PT segments into the germ line of a non-human mammal and collecting milk
 PT from female progeny.
 PT
 XX Disclosure; (Page 55-57; 99pp; English.
 PS
 XX Human fibrinogen B-beta chain may be produced recombinantly, preferably
 CC by sheep beta-lactoglobulin signal peptide fusion protein gene expression
 CC in non-human transgenic animal milk, preferably of a sheep, pig, goat or
 CC cattle. Co-expression with the fibrinogen A-alpha chain (see AAR82244)
 CC and the gamma chain (see AAR82245) results in the production of active
 CC fibrinogen, which is useful in human and veterinary medicine, e.g. in the
 CC formulation of surgical adhesives, which also consist of Factor-XIII, and
 CC as a coating surface for polymeric articles, such as synthetic vascular
 CC grafts
 CC
 XX
 XX Sequence 491 AA;
 SQ
 Query Match 100.0%; Score 116; DB 2; Length 491;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWSYMRKMSMKIRPFFPQQ 21
 |||||
 Db 471 KGSWSYMRKMSMKIRPFFPQQ 491
 RESULT 7
 AAM78492
 ID AAM78492 standard; protein; 491 AA.
 XX
 AC AAM78492;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1154.
 XX
 DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 XX Homo sapiens.
 OS

XX
 PN W0200157190-A2.
 XX
 XX 09-AUG-2001.
 PD
 XX
 XX 05-FEB-2001; 2001WO-US004098.
 PF
 XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Zhang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAK51625.
 DR
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 PT
 XX Claim 20; Page 3389-3390; 6221pp; English.
 PS
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 XX Sequence 491 AA;
 SQ
 Query Match 100.0%; Score 116; DB 4; Length 491;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWSYMRKMSMKIRPFFPQQ 21
 |||||
 Db 471 KGSWSYMRKMSMKIRPFFPQQ 491
 RESULT 8
 AAE36413
 ID AAE36413 standard; protein; 491 AA.
 XX
 AC AAE36413;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Human F8G reference protein (GI 11761631).
 XX
 DE Thrombospondin 2; THBS2; angiotensin converting enzyme; polymorphism;
 KW ACE-1; beta-fibrinogen; FGB; peripheral vascular disease; ischaemia;
 KW vascular disease; myocardial infarction; pulmonary embolism; stroke;
 KW atherosclerosis; coronary artery disease; venous thromboembolism; human.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH

FT Misc-difference 478
 FT /note= "This residue is changed to Lys due to single
 FT nucleotide polymorphism (SNP)"
 XX
 PN WO2003020118-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 04-SEP-2002; 2002WO-US028113.
 XX
 PR 05-SEP-2001; 2001US-0317178P.
 PR 16-OCT-2001; 2001US-0329958P.
 PR 14-DEC-2001; 2001US-00017724.
 XX
 XX (VITI-) VITIVITY INC.
 XX
 XX McCarthy J;
 PI
 DR WPI; 2003-300816/29.
 XX
 XX Identifying polymorphisms in thrombospondin 2, angiotensin converting
 PT enzyme and/or beta-fibrinogen genes in nucleic acid sample of subject, by
 PT contacting the nucleic acid with a complementary probe or primer.
 XX
 PS Claim 5; Fig 6; 194pp; English.
 XX
 CC The invention relates to a method for determining the identity of one or
 CC more allelic variants of a polymorphic region of a thrombospondin 2
 CC (THBS2), angiotensin converting enzyme (ACE)-1 and/or beta-fibrinogen
 CC (FGB) genes in a nucleic acid obtained from a subject. The method
 CC involves contacting the nucleic acid with a complementary probe or
 CC primer. The method is useful for diagnosing or aiding in the diagnosis of
 CC vascular disease or disorder in a subject e.g. myocardial infarction,
 CC coronary artery disease, atherosclerosis, ischaemia, stroke, peripheral
 CC vascular disease, venous thromboembolism and pulmonary embolism. The
 CC present sequence is human FBG reference protein. Note: This sequence is
 CC said to be encoded by SEQ ID NO: 5 (AAD55117). However this does not
 CC appear to be the case
 XX
 XX Sequence 491 AA;
 SQ
 Query Match 100.0%; Score 116; DB 6; Length 491;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKMSMKIRPFPQQ 21
 DB 471 KGSWYSMRKMSMKIRPFPQQ 491
 RESULT 9
 ADP65229
 ID ADP65229 standard; protein; 491 AA.
 XX
 AC ADP65229;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human fibrinogen, beta chain preproprotein, fibrinogen, B beta protein.
 XX
 KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigen; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072827-A1.
 XX
 XX 04-SEP-2003.
 PD

PF 31-OCT-2002; 2002WO-US035433.
 XX
 PR 31-OCT-2001; 2001US-0336220P.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Hirsch R, Thorton SL;
 XX
 DR WPI; 2003-712740/67.
 DR GENBANK; NP_005132.
 XX
 FT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX
 PS Disclosure; Page; 56pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritis. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritis in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritis, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritis. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.
 XX
 SQ Sequence 491 AA;
 Query Match 100.0%; Score 116; DB 7; Length 491;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKMSMKIRPFPQQ 21
 DB 471 KGSWYSMRKMSMKIRPFPQQ 491
 RESULT 10
 ADP65300
 ID ADP65300 standard; protein; 491 AA.
 XX
 AC ADP65300;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human fibrinogen, beta chain preproprotein.
 XX
 KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigen; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX

OS Homo sapiens.
 XX WO2003072827-A1.
 XX
 XX 04-SEP-2003.
 XX
 XX 31-OCT-2002; 2002WO-US035433.
 XX
 XX 31-OCT-2001; 2001US-0336220P.
 XX
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 XX Hirsch R, Thorton SL;
 XX WPI; 2003-712740/67.
 XX GENBANK; NP_005132.
 XX
 XX Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX
 XX Disclosure; Page; 56pp; English.
 XX
 XX The invention relates to a novel method for diagnosing and analysing a
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.
 XX
 XX SQ Sequence 491 AA;
 Query Match 100.0%; Score 116; DB 7; Length 491;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKMSKIRPFPPQQ 21
 Db 471 KGSWYSMRKMSKIRPFPPQQ 491
 RESULT 11
 AAU31380
 ID AAU31380 standard; protein; 502 AA.
 XX
 XX AAU31380;
 AC
 XX 18-DEC-2001 (first entry)
 DT
 XX Novel human secreted protein #1871.
 DE
 XX Human; vaccination; gene therapy; nutritional supplement;
 KW

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 XX Homo sapiens.
 XX
 XX WO200179449-A2.
 XX
 XX 25-OCT-2001.
 XX
 XX 16-APR-2001; 2001WO-US008656.
 XX
 XX 18-APR-2000; 2000US-00552929.
 XX
 XX 26-JAN-2001; 2001US-00770160.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-611725/70.
 XX
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 PT
 XX
 XX Claim 20; Page 430; 765pp; English.
 XX
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 XX SQ Sequence 502 AA;
 Query Match 100.0%; Score 116; DB 4; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.9e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKMSKIRPFPPQQ 21
 Db 482 KGSWYSMRKMSKIRPFPPQQ 502
 RESULT 12
 AAU78491
 ID AAU78491 standard; protein; 539 AA.
 XX
 XX AAU78491;
 AC
 XX 06-NOV-2001 (first entry)
 DT
 XX Human protein SEQ ID NO 1153.
 DE
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 XX Homo sapiens.
 XX
 XX WO200157190-A2.
 XX

PD 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US004098.
 PF 03-FEB-2000; 2000US-00496914.
 XX 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAKS1624.
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX Claim 20; Page 3388-3389; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 539 AA;
 Query Match 100.0%; Score 116; DB 4; Length 539;
 Best Local Similarity 100.0%; Pred. No. 3.1e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KGSWYSMRKMSMKIRPFPFQQ 21
 Db 519 KGSWYSMRKMSMKIRPFPFQQ 539
 RESULT 13
 ADE76868
 ID ADE76868 standard; protein; 488 AA.
 AC ADE76868;
 XX 29-JAN-2004 (first entry)
 XX Human protein expressed in a liver disorder #11.
 XX human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
 KW tumour; liver; inflammatory disorder; immune response disorder;
 KW high-throughput screening; differential gene expression; gene therapy.
 XX
 OS Homo sapiens.
 XX US2003108871-A1.
 PN 12-JUN-2003.
 PD 30-JUL-2001; 2001US-00919039.
 PF

XX 28-JUL-2000; 2000US-0222113P.
 XX (KASE/) KASER M R.
 PA Kaser MR;
 PI WPI; 2004-031227/03.
 XX N-PSDB; ADE76867.
 DR Composition comprising several cDNAs that are differentially expressed in
 PT treated human C3A liver cell cultures, useful for treating liver
 PT disorders.
 XX Claim 1; SEQ ID NO 33; 41pp; English.
 XX The invention relates to a composition comprising several cDNAs that are
 CC differentially expressed in a liver disorder. The composition is useful
 CC for treating liver disorder such as hyperlipidaemia, hypertension, type
 CC II diabetes, tumours of the liver and disorders of the inflammatory and
 CC immune response. The composition is useful for a high-throughput method
 CC of screening several molecules or compounds to identify a ligand which
 CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
 CC high-throughput method for using a protein to screen several molecules or
 CC compounds to identify at least one ligand which specifically binds the
 CC protein which involves combining the protein encoded by the cDNA with
 CC several of molecules or compounds under conditions to allow specific
 CC binding, and detecting specific binding between the protein and a
 CC molecule or compound, therefore identifying a ligand which specifically
 CC binds the protein. The composition is useful for detecting and
 CC quantifying differential gene expression, can be used in gene therapy, to
 CC formulate prognosis and to design a treatment regimen and to monitor the
 CC efficacy of treatment. The present sequence represents the amino acid
 CC sequence of a protein encoded by a cDNA differentially expressed in a
 CC liver disorder.
 XX
 SQ Sequence 488 AA;
 Query Match 97.4%; Score 113; DB 8; Length 488;
 Best Local Similarity 95.2%; Pred. No. 8.8e-10;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KGSWYSMRKMSMKIRPFPFQQ 21
 Db 468 KGSWYSMRKMSMKIRPFPFQQ 488
 RESULT 14
 AAM79475
 ID AAM79475 standard; protein; 495 AA.
 XX AAM79475;
 XX 06-NOV-2001 (first entry)
 XX Human protein SEQ ID NO 3121.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX WO200157190-A2.
 PN 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US004098.
 PF 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR

PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAKS2608.
 DR
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 PT
 XX
 PS Claim 20; Page 257-258; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 495 AA;

Query Match 97.4%; Score 113; DB 4; Length 495;
 Best Local Similarity 95.2%; Pred. No. 8.9e-10;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKMSMKIRPFPPQQ 21
 |||||:|||||||
 Db 475 KGSWYSMKKMSMKIRPFPPQQ 495
 RESULT 15
 AAM79476
 ID AAM79476 standard; protein; 495 AA.
 XX
 AC AAM79476;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3122.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAKS2609.
 DR
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 PT
 XX
 PS Claim 20; Page 258; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 495 AA;

Query Match 97.4%; Score 113; DB 4; Length 495;
 Best Local Similarity 95.2%; Pred. No. 8.9e-10;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKMSMKIRPFPPQQ 21
 |||||:|||||||
 Db 475 KGSWYSMKKMSMKIRPFPPQQ 495
 RESULT 16
 AAM79477
 ID AAM79477 standard; protein; 495 AA.
 XX
 AC AAM79477;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3123.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.


```
SQ Sequence 491 AA;
Query Match          94.0%; Score 109; DB 7; Length 491;
Best Local Similarity 95.2%; Pred. No. 4e-09;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGSWYSMRKSMKIRPFPPQ 21
    |||||
Db 471 KGSWYSMRKSMKDRPFPPQ 491

RESULT 19
ADI82107
ID ADI82107 standard; protein; 479 AA.
XX
AC ADI82107;
XX
DT 22-APR-2004 (first entry)
XX
DE Fibrinogen-beta-chain protein.
XX
KW kidney toxicity; T-kininogen; inter-alpha-inhibitor H4P heavy chain;
KW alpha-1-macroglobulin; apolipoprotein E; clusterin; complement C3;
KW complement C4; fibrinogen-alpha-chain; fibrinogen-beta-chain;
KW plasma retinol binding protein; renal tubular necrosis; drug development.
XX
OS Unidentified.
XX
PN WO2004005934-A2.
XX
PD 15-JAN-2004.
XX
PF 04-JUL-2003; 2003WO-GB002893.
XX
PR 04-JUL-2002; 2002GB-00015575.
PR 09-SEP-2002; 2002GB-00020879.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Ranasinghe-Bandara L;
XX
DR WPI; 2004-099412/10.
XX
PT Screening or diagnosing kidney toxicity, useful in monitoring
PT effectiveness of treatment for kidney toxicity or for screening and
PT developing of drugs, by detecting and quantifying T-kininogen and inter-
PT alpha-inhibitor H4P heavy chain.
XX
PS Disclosure; SEQ ID NO 10; 41pp; English.
XX
CC The invention comprises a method for screening or diagnosing kidney
CC toxicity. The method involves the use of the following proteins: T-
CC kininogen, inter-alpha-inhibitor H4P heavy chain, alpha-1-macroglobulin,
CC apolipoprotein E, clusterin, complement C3, complement C4, fibrinogen-
CC alpha-chain, fibrinogen-beta-chain, and plasma retinol binding protein.
CC The method of the invention is useful in screening or diagnosing kidney
CC toxicity (e.g. renal tubular necrosis). The method is also useful for
CC monitoring the effectiveness of treatment for kidney toxicity and for
CC screening and developing drugs. The present amino acid sequence
CC represents a protein that was used in the exemplification of the
XX invention.
XX
SQ Sequence 479 AA;
Query Match          91.4%; Score 106; DB 8; Length 479;
Best Local Similarity 90.5%; Pred. No. 1.2e-08;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGSWYSMRKSMKIRPFPPQ 21
    |||||
Db 459 KGSWYSMRKSMKIRPFVFPQ 479

RESULT 20
AAM97040
ID AAM97040 standard; peptide; 14 AA.
XX
AC AAM97040;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #315 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Disclosure; Page 3737; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX
SQ Sequence 14 AA;
Query Match          64.7%; Score 75; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSWYSMRKSMKIR 15
    |||||
Db 1 GSWYSMRKSMKIR 14

RESULT 21
AAM97039
ID AAM97039 standard; peptide; 14 AA.
```



```

XX AC AAM97039;
XX DT 24-JAN-2002 (first entry)
XX DE Human peptide #314 encoded by a SNP oligonucleotide.
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
XX KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX KW complement related protein; cytochrome; kinesin; cytokine; interferon;
XX KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX KW multifactorial disease; autoimmune disease; infection;
XX KW nervous system disease.
XX OS Homo sapiens.
XX FN WO200147944-A2.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000WO-US035498.
XX PR 28-DEC-1999; 99US-0173419P.
XX PR 27-DEC-2000; 2000US-00173419.
XX PA (CURA-) CURAGEN CORP.
XX FI Shimkets RA, Leach M;
XX DR WPI; 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX PT autoimmune diseases and infections.
XX PS Disclosure; Page 3736; 4143pp; English.
XX CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
XX CC encoding polymorphic variants of proteins related to amylases, amyloid
XX CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
XX CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
XX CC complement related proteins, cytochromes, kinesins, cytokines,
XX CC interferons, interleukins, G-protein coupled receptors and thioesterases.
XX CC The present sequence is a peptide encoded by one such oligonucleotide.
XX CC The oligonucleotides and the peptides encoded by them may be used in the
XX CC prevention, diagnosis and treatment of diseases associated with
XX CC inappropriate expression of the proteins listed above. Disorders that may
XX CC be prevented, diagnosed and/or treated include multifactorial diseases
XX CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
XX CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
XX CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
XX CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
XX CC system and an infection of pathogenic organisms
XX SQ Sequence 14 AA;
XX Query Match 64.7%; Score 75; DB 4; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 2 GSWYSMRKMSMKIR 15
XX Db 1 GSWYSMRKMSMKIR 14
XX RESULT 22
XX AAM00113
XX ID AAM00113 standard; peptide; 14 AA.
XX AC AAM00113;
XX XX

```

```

DT 01-OCT-2001 (first entry)
XX Human angiopoietin fragment SEQ ID NO: 653.
DE
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.
XX OS Homo sapiens.
XX PN WO200151670-A2.
XX PD 19-JUL-2001.
XX PF 05-JAN-2001; 2001WO-US000322.
XX PR 07-JAN-2000; 2000US-0174962P.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach MD;
XX DR WPI; 2001-451871/48.
XX DR N-PSDB; AAH89222.
XX CC Isolated human polynucleotides containing single nucleotide
XX CC polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX CC infection and diabetes.
XX PS Disclosure; Page 293; 475pp; English.
XX CC The present invention relates to human nucleic acids containing single
XX CC nucleotide polymorphisms (SNPs). These can be used in forensic and
XX CC paternity tests, and to aid in the treatment of diseases associated with
XX CC aberrant protein expression, including cancer, amyloidosis, diabetes,
XX CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
XX CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
XX CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
XX CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX CC autoimmunity. The present sequence is a peptide encoded by a
XX CC polymorphism-containing oligonucleotide fragment of the invention
XX SQ Sequence 14 AA;
XX Query Match 64.7%; Score 75; DB 4; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 2 GSWYSMRKMSMKIR 15
XX Db 1 GSWYSMRKMSMKIR 14
XX RESULT 23
XX AAM00114
XX ID AAM00114 standard; peptide; 14 AA.
XX AC AAM00114;
XX AC AAM00114;
XX DT 01-OCT-2001 (first entry)
XX DE Human angiopoietin fragment SEQ ID NO: 654.
XX KW Human; single nucleotide polymorphism; SNP; paternity test;
XX KW forensic test; aberrant protein expression.
XX OS Homo sapiens.
XX PN WO200151670-A2.
XX PD 19-JUL-2001.
XX PF 05-JAN-2001; 2001WO-US000322.

```

XX 07-JAN-2000; 2000US-0174962P.
 XX (CURA-) CURAGEN CORP.
 XX Shimkets RA, Leach MD;
 XX WPI; 2001-451871/48.
 XX N-PSDB; AAH89223.
 XX
 PT Isolated human polynucleotides containing single nucleotide
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes.
 XX
 PS Disclosure; Page 293; 475pp; English.
 XX
 CC The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with
 CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a peptide encoded by a
 CC polymorphism-containing oligonucleotide fragment of the invention
 XX
 SQ Sequence 14 AA;
 Query Match 62.1%; Score 72; DB 4; Length 14;
 Best Local Similarity 92.9%; Pred. No. 0.0001;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GSWYSMRKMSMKIR 15
 Db 1 GSWYSMRKMSMKIR 14
 RESULT 24
 AAG65026
 ID AAG65026 standard; peptide; 16 AA.
 XX
 AC AAG65026;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Haptotactic peptide consensus sequence #1.
 XX
 KW Human; cell attachment peptide; haptotactic; fibrinogen; wound healing;
 KW angiotensin; tenascin; microfibril-associated glycoprotein-4; MFAP4;
 KW cell separation; cell receptor.
 XX
 OS Unidentified.
 XX
 PN WO200153324-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 21-JAN-2001; 2001WO-IL000057.
 XX
 PR 20-JAN-2000; 2000US-00487790.
 XX
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 XX
 PI Marx G, Gorodetsky R;
 XX WPI; 2001-457595/49.
 XX
 XX Novel haptotactic peptides useful for enhancing wound healing and
 PT osteogenesis.
 XX
 PS Claim 6; Page 7; 43pp; English.

XX The present invention provides haptotactic peptides with sequences
 CC homologous to sequences found within the C-termini of fibrinogen, and
 CC which are characterised by their ability to induce cell attachment to a
 CC surface to which the peptide is bound. These are useful in the treatment
 CC of wounds and diseases, to separate different types of cells in culture,
 CC to analyse cell receptor mechanisms and to design peptide-derivatised
 CC drugs. The present sequence is a consensus sequence of haptotactic
 CC peptides
 XX
 SQ Sequence 16 AA;
 Query Match 51.7%; Score 60; DB 4; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.011;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKMSMKIRP 16
 Db 1 KGSWYSMRKMSMKIRP 16
 RESULT 25
 ADO85142
 ID ADO85142 standard; peptide; 16 AA.
 XX
 AC ADO85142;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human-derived consensus haptotactic peptide SeqID13.
 XX
 KW haptotactic; liposomal composition; carboxy termini; fibrinogen chain;
 KW liposome; lipid bilayer; aqueous compartment; delivery; human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3 /label= OTHER
 FT /note= "OTHER= Non-charged amino acid or optionally
 FT absent"
 FT Misc-difference 4 /label= OTHER
 FT /note= "OTHER= Non-charged amino acid or optionally
 FT absent"
 FT Misc-difference 10 /label= OTHER
 FT /note= "OTHER= Non-charged amino acid or optionally
 FT absent"
 FT Misc-difference 11 /label= OTHER
 FT /note= "OTHER= Non-charged amino acid or optionally
 FT absent"
 XX
 PN WO2004041298-A1.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003WO-IL0000911.
 XX
 PR 03-NOV-2002; 2002IL-00152609.
 XX
 PA (HAPT-) HAPTO BIOTECH INC.
 XX
 PI Marx G, Gorodetsky R;
 XX WPI; 2004-449501/42.
 XX
 XX Haptotactic peptide liposomal composition, useful for enhancing liposome
 PT uptake into cells, comprising peptide capable of eliciting cell
 PT attachment responses and sequence similarity to haptotactic peptides and
 PT liposome having lipid bilayers.

XX PS Claim 6; SEQ ID NO 13; 53pp; English.

XX CC This invention relates to a novel haptotactic peptide liposomal

XX CC composition, which comprises at least one type of peptide and one type of

XX CC liposome, where the peptide elicits cell attachment responses and has an

XX CC amino acid sequence that is at least 60% homologous to a haptotactic

XX CC peptide present within the carboxy termini of fibrinogen chains, and the

XX CC liposome has at least one lipid bilayer enclosing an aqueous compartment.

XX CC The invention is useful for enhancing liposome uptake into cells or for

XX CC enhancing intracellular uptake of biologically active compounds by low-

XX CC permeability through the cell membrane using a haptotactic-peptide

XX CC liposomal composition. The invention may be particularly useful for

XX CC enhancing the delivery of pharmaceutical agent into cells, for enhancing

XX CC the delivery of diagnostic agent into cells or for enhancing delivery of

XX CC cosmetically effective liposomes into cells, where the liposomes of the

XX CC composition have a cosmetic beneficial effect. The present sequence is

XX CC that of a human-derived haptotactic peptide which may be used during the

XX CC creation of the compositions of the invention.

XX SQ Sequence 16 AA;

Query Match 51.7%; Score 60; DB 8; Length 16;

Best Local Similarity 75.0%; Pred. No. 0.011;

Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKXSMKIRP 16

Db 1 KGXXYSMRKXSMKIRP 16

RESULT 26

AAG65016

ID AAG65016 standard; peptide; 20 AA.

XX AC AAG65016;

XX DT 01-OCT-2001 (first entry)

XX DE Human fibrinogen C-terminus homologue preCgamma.

XX KW Human; cell attachment peptide; haptotactic; fibrinogen; wound healing;

XX KW angiotensin; tenascin; microfibril-associated glycoprotein-4; MFAP4;

XX KW cell separation; cell receptor.

XX OS Unidentified.

XX PN WO200153324-A2.

XX PD 26-JUL-2001.

XX PF 21-JAN-2001; 2001WO-IL0000057.

XX PR 20-JAN-2000; 2000US-00487790.

XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX PI Marx G, Gorodetsky R;

XX DR WPT; 2001-457595/49.

XX PT Novel haptotactic peptides useful for enhancing wound healing and

XX FT osteogenesis.

XX PS Claim 3; Page 6; 43pp; English.

XX CC The present invention provides haptotactic peptides with sequences

XX CC homologous to sequences found within the C-termini of fibrinogen, and

XX CC which are characterised by their ability to induce cell attachment to a

XX CC surface to which the peptide is bound. These are useful in the treatment

XX CC of wounds and diseases, to separate different types of cells in culture,

XX CC to analyse cell receptor mechanisms and to design peptide-derivatised

XX CC drugs. The present sequence is a homologue of a human fibrinogen C-

CC terminal peptide

XX SQ Sequence 20 AA;

Query Match 51.7%; Score 60; DB 4; Length 20;

Best Local Similarity 64.7%; Pred. No. 0.014;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKXSMKIRP 17

Db 1 KTRWYSMKTKTKIRP 17

RESULT 27

AD085132

ID AD085132 standard; peptide; 20 AA.

XX AC AD085132;

XX DT 12-AUG-2004 (first entry)

XX DE Human-derived haptotactic peptide SeqID3.

XX KW haptotactic; liposomal composition; carboxy termini; fibrinogen chain;

XX KW liposome; lipid bilayer; aqueous compartment; delivery; human.

XX OS Homo sapiens.

XX PN WO2004041298-A1.

XX PD 21-MAY-2004.

XX PF 03-NOV-2003; 2003WO-IL000911.

XX PR 03-NOV-2002; 2002IL-00152609.

XX PA (HAPT-) HAPTO BIOTECH INC.

XX PI Marx G, Gorodetsky R;

XX DR WPI; 2004-449501/42.

XX PT Haptotactic peptide liposomal composition, useful for enhancing liposome

XX PT uptake into cells, comprising peptide capable of eliciting cell

XX PT attachment responses and sequence similarity to haptotactic peptides and

XX PT liposome having lipid bilayers.

XX PS Claim 3; SEQ ID NO 3; 53pp; English.

XX CC This invention relates to a novel haptotactic peptide liposomal

XX CC composition, which comprises at least one type of peptide and one type of

XX CC liposome, where the peptide elicits cell attachment responses and has an

XX CC amino acid sequence that is at least 60% homologous to a haptotactic

XX CC peptide present within the carboxy termini of fibrinogen chains, and the

XX CC liposome has at least one lipid bilayer enclosing an aqueous compartment.

XX CC The invention is useful for enhancing liposome uptake into cells or for

XX CC enhancing intracellular uptake of biologically active compounds by low-

XX CC permeability through the cell membrane using a haptotactic-peptide

XX CC liposomal composition. The invention may be particularly useful for

XX CC enhancing the delivery of pharmaceutical agent into cells, for enhancing

XX CC the delivery of diagnostic agent into cells or for enhancing delivery of

XX CC cosmetically effective liposomes into cells, where the liposomes of the

XX CC composition have a cosmetic beneficial effect. The present sequence is

XX CC that of a human-derived haptotactic peptide which may be used during the

XX CC creation of the compositions of the invention.

XX SQ Sequence 20 AA;

Query Match 51.7%; Score 60; DB 8; Length 20;

Best Local Similarity 64.7%; Pred. No. 0.014;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKXSMKIRP 17

Db 1 KTRWYSMKTKTKIIPF 17
| | | | | : | | | | |
RESULT 28
AAB39176
ID AAB39176 standard; protein; 194 AA.
XX
AC AAB39176;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human secreted protein BLAST search protein SEQ ID NO: 143.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200058513-A1.
XX
PD 05-OCT-2000.
XX
PF 22-MAR-2000; 2000WO-US007506.
XX
PR 26-MAR-1999; 99US-0126505P.
XX
PR 17-DEC-1999; 99US-0172412P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-594649/56.
XX
PT Forty-nine polynucleotide sequences, and their encoded secreted
PT polypeptides, used in the treatment and diagnosis of cancers, autoimmune
PT disorders, and skin disorders.
XX
PS Disclosure; Page 407; 413pp; English.
XX
CC The invention relates to the isolation of genes AAC73865-C73913 encoding
CC the human secreted proteins AAB39093-B39141. This sequence represents a
CC peptide fragment homologous to the protein encoded by the gene isolated
CC in the present invention. The sequence is a search result from a BLASTX
CC homology search. The genes and proteins are useful for preventing,
CC ameliorating or treating medical conditions, e.g. by protein or gene
CC therapy. The genes are isolated from a range of human tissues disclosed
CC in the specification. The nucleic acids, proteins, antibodies and
CC (ant)agonists are useful in the diagnosis, treatment and prevention of:
CC (a) cancer, e.g. breast and ovarian cancer, and other cancers of the
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
CC bacterial, fungal and parasitic infections
XX
SQ Sequence 194 AA;
Query Match 51.7%; Score 60; DB 3; Length 194;
Best Local Similarity 64.7%; Pred. No. 0.15;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 KGSWYSMRKMSMKIRPF 17
| | | | | : | | | | |
Db 156 KTRWYSMKTKTKIIPF 172

RESULT 29
AAB39177
ID AAB39177 standard; protein; 194 AA.
XX
AC AAB39177;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human secreted protein BLAST search protein SEQ ID NO: 144.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200058513-A1.
XX
PD 05-OCT-2000.
XX
PF 22-MAR-2000; 2000WO-US007506.
XX
PR 26-MAR-1999; 99US-0126505P.
XX
PR 17-DEC-1999; 99US-0172412P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-594649/56.
XX
PT Forty-nine polynucleotide sequences, and their encoded secreted
PT polypeptides, used in the treatment and diagnosis of cancers, autoimmune
PT disorders, and skin disorders.
XX
PS Disclosure; Page 407-408; 413pp; English.
XX
CC The invention relates to the isolation of genes AAC73865-C73913 encoding
CC the human secreted proteins AAB39093-B39141. This sequence was used as a
CC query sequence for doing BLASTX searches to determine homologous
CC sequences to the protein isolated in the present invention. The genes and
CC proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)
CC immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections
XX
SQ Sequence 194 AA;
Query Match 51.7%; Score 60; DB 3; Length 194;
Best Local Similarity 64.7%; Pred. No. 0.15;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 KGSWYSMRKMSMKIRPF 17
| | | | | : | | | | |
Db 156 KTRWYSMKTKTKIIPF 172

RESULT 30
ADK70498

ID ADK70498 standard; protein; 437 AA.
AC ADK70498;
XX
DT 06-MAY-2004 (first entry)
XX
DE Respiratory disease differentially expressed protein #64.
XX
KW cytosolic; respiratory; antiasthmatic; gene therapy;
KW differential gene expression; respiratory disorder; lung cancer;
KW chronic obstructive pulmonary disease; emphysema; asthma.
XX
OS Homo sapiens.
XX
PN WO2003101283-A2.
XX
PD 11-DEC-2003.
XX
PF 02-JUN-2003; 2003WO-US017409.
XX
PR 04-JUN-2002; 2002US-0386005P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Rickert PK, Kraenow R;
XX
DR WPI; 2004-042945/04.
XX
PT New combination comprising cDNAs and proteins that are differentially
PT expressed in respiratory disorders, useful for diagnosing or treating
PT respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
PT diseases or asthma.
XX
PS Claim 14; SEQ ID NO 234; 343pp; English.
XX
CC The invention relates to cDNA sequences that are differentially expressed
CC in respiratory disorders or their complements or encoded proteins. The
CC cDNAs and proteins are useful for diagnosing, treating or monitoring
CC treatment of a subject with a respiratory disease including lung cancer,
CC chronic obstructive pulmonary diseases, emphysema or asthma. The protein
CC is also useful for screening molecules or compounds to identify at least
CC one ligand which specifically binds the protein. It is also useful for
CC preparing and purifying a polyclonal or monoclonal antibody. This
CC sequence corresponds to a protein of the invention.
XX
SQ Sequence 437 AA;
Query Match 51.7%; Score 60; DB 8; Length 437;
Best Local Similarity 64.7%; Pred. No. 0.37;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 KGSWYSMRKMSMKIRPF 17
Db 399 KTRWYSMKTKTKIIPF 415
RESULT 31
ADL61247
ID ADL61247 standard; protein; 437 AA.
AC ADL61247;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human protein tyrosine kinase biomarker fibrinogen gamma protein.
XX
KW predictor set; protein tyrosine kinase; cytosolic; antiangiogenic;
KW vasotrophic; vulnery; pharmacogenomic; drug sensitivity; breast cancer;
KW hypervascular disease; angiogenesis; wound healing scar; human;
KW biomarker; fibrinogen gamma.
XX
OS Homo sapiens.
XX

PN WO2004020583-A2.
XX
PD 11-MAR-2004.
XX
PF 26-AUG-2003; 2003WO-US026491.
XX
PR 27-AUG-2002; 2002US-0406385P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Huang F, Han X, Reeves KA, Amler L, Fairchild CR, Lee FY;
PI Shaw P;
XX
DR WPI; 2004-239171/22.
DR N-PSDB; ADL61110.
XX
PT New predictor sets with a plurality of polynucleotides and/or
PT polypeptides whose expression pattern predicts cell response to a
PT compound that modulates protein tyrosine kinase activity, useful in
PT treating breast cancer.
XX
PS Claim 9; SEQ ID NO 171; 649pp; English.
XX
CC The invention relates to a novel predictor set comprising a plurality of
CC polynucleotides and/or polypeptides whose expression pattern is
CC predictive of the response of cells to treatment with a compound that
CC modulates protein tyrosine kinase activity or members of the protein
CC tyrosine kinase pathway. The molecules of the invention demonstrate
CC cytosolic, antiangiogenic, vasotrophic and vulnery activities and may
CC be useful in the field of pharmacogenomics, in particular for determining
CC drug sensitivity and in treating breast cancer, hypervascular diseases,
CC angiogenesis and scars in wound healing. The current sequence is that of
CC a human protein tyrosine kinase biomarker protein of the invention.
XX
SQ Sequence 437 AA;
Query Match 51.7%; Score 60; DB 8; Length 437;
Best Local Similarity 64.7%; Pred. No. 0.37;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 KGSWYSMRKMSMKIRPF 17
Db 399 KTRWYSMKTKTKIIPF 415
RESULT 32
AAR82246
ID AAR82246 standard; protein; 453 AA.
XX
AC AAR82246;
XX
DT 27-OCT-1996 (first entry)
XX
DE Human fibrinogen gamma' chain protein.
XX
KW Human fibrinogen gamma' chain; transgenic animal milk; treatment;
KW sheep beta-lactoglobulin signal peptide fusion protein;
KW surgical adhesive.
XX
OS Homo sapiens.
XX
PN WO9523868-A1.
XX
PD 08-SEP-1995.
XX
PF 01-MAR-1995; 95WO-US002648.
XX
PR 03-MAR-1994; 94US-00206176.
XX
PA (ZYMO) ZYMOGENETICS INC.
PA (PHAR-) PHARM PROTEINS LTD.
XX
PI Garner I, Dalrymple MA, Prunkard DE, Foster DC;

XX WPI; 1995-320582/41.
 DR N-PSDB; AAT03854.
 XX
 PT Production of fibrinogen in transgenic mammals - by introducing DNA
 PT segments into the germ line of a non-human mammal and collecting milk
 PT from female progeny.
 XX
 PS Disclosure; Page 67-69; 99pp; English.
 XX
 CC The alternatively spliced human fibrinogen gamma' protein is produced by
 CC alternative splicing at nucleotides 9511 and 10054 of AAT03854 resulting
 CC in translation terminating after nucleotide 10065. Human fibrinogen
 CC gamma' chain may be produced recombinantly, preferably by sheep beta-
 CC lactoglobulin signal peptide fusion protein gene expression in non-human
 CC transgenic animal milk, preferably of a sheep, pig, goat or cattle. Co-
 CC expression with the fibrinogen A-alpha chain (see AAR82244) and the B-
 CC beta chain (see AAR82243) results in the production of active fibrinogen,
 CC which is useful in human and veterinary medicine, e.g. in the formulation
 CC of surgical adhesives, which also consist of Factor-XIII, and as a
 CC coating surface for polymeric articles, such as synthetic vascular grafts
 XX
 SQ Sequence 453 AA;
 Query Match 51.7%; Score 60; DB 2; Length 453;
 Best Local Similarity 64.7%; Pred. No. 0.38;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKSMKIRPF 17
 | | | | | : | | | |
 Db 399 KTRWYSMKTKTKIIPF 415
 RESULT 33
 AAR82245
 ID AAR82245 standard; protein; 453 AA.
 XX
 AC AAR82245;
 XX
 DT 26-OCT-1996 (first entry)
 XX
 DE Human fibrinogen gamma chain protein.
 XX
 KW Human fibrinogen gamma chain; transgenic animal milk; treatment;
 KW sheep beta-lactoglobulin signal peptide fusion protein;
 KW surgical adhesive.
 XX
 OS Homo sapiens.
 XX
 PN WO9523868-A1.
 XX
 PD 08-SEP-1995.
 XX
 PF 01-MAR-1995; 95WO-US002648.
 XX
 PR 03-MAR-1994; 94US-00206176.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 PA (PHAR-) PHARM PROTEINS LTD.
 XX
 PI Garner I, Dalrymple MA, Prunkard DE, Foeter DC;
 XX
 DR WPI; 1995-320582/41.
 DR N-PSDB; AAT03854.
 XX
 PT Production of fibrinogen in transgenic mammals - by introducing DNA
 PT segments into the germ line of a non-human mammal and collecting milk
 PT from female progeny.
 XX
 PS Disclosure; Page 58-67; 99pp; English.
 XX
 CC Human fibrinogen gamma chain may be produced recombinantly, preferably by
 CC sheep beta-lactoglobulin signal peptide fusion protein gene expression in

CC non-human transgenic animal milk, preferably of a sheep, pig, goat or
 CC cattle. Co-expression with the fibrinogen A-alpha chain (see AAR82244)
 CC and the B-beta chain (see AAR82243) results in the production of active
 CC fibrinogen, which is useful in human and veterinary medicine, e.g. in the
 CC formulation of surgical adhesives, which also consist of Factor-XIII, and
 CC as a coating surface for polymeric articles, such as synthetic vascular
 CC grafts
 XX
 SQ Sequence 453 AA;
 Query Match 51.7%; Score 60; DB 2; Length 453;
 Best Local Similarity 64.7%; Pred. No. 0.38;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKSMKIRPF 17
 | | | | | : | | | |
 Db 399 KTRWYSMKTKTKIIPF 415
 RESULT 34
 ADD45364
 ID ADD45364 standard; protein; 453 AA.
 XX
 AC ADD45364;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P02679, SEQ ID NO 10797.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 PA (PARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; P02679.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 453 AA;
 Query Match 51.7%; Score 60; DB 7; Length 453;
 Best Local Similarity 64.7%; Pred. No. 0.38;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPF 17
 | | | | | : | | | | |
 Db 399 KTRWYSMKTKTKIIPF 415

RESULT 35
 ID ADQ30579 standard; protein; 453 AA.

XX AC ADQ30579;

XX DT 23-SEP-2004 (first entry)

XX DE Pancreas cancer marker - fibrinogen gamma chain precursor.

XX KW Cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;
 KW differential expression.

XX OS Homo sapiens.

XX PN WO2004055519-A2.

XX PD 01-JUL-2004.

XX PF 11-DEC-2003; 2003WO-EP014057.

XX PR 17-DEC-2002; 2002EP-00028058.

XX PR 05-NOV-2003; 2003EP-00025237.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.

XX PI Chen J, Hu L, Liu TH, Lu ZH, Shen Y;

XX DR WPI; 2004-488121/46.

XX PT New specific markers comprises at least one polypeptide up-regulated in
 PT pancreatic cancer, useful for diagnosing pancreatic cancer.

XX PS Claim 1; SEQ ID NO 66; 381pp; English.

XX CC The invention relates to a marker (I) for diagnosis of pancreatic cancer
 CC comprising at least one polypeptide selected from 55 proteins up-
 CC regulated in pancreatic cancer (Table 2 and Table 3, given in the
 CC specification) or from 68 proteins with higher levels in pancreatic
 CC cancer compared to normal tissue (Table 6, given in the specification).
 CC (I) is a polypeptide for use as a marker or as a component of a marker
 CC for diagnosis of pancreatic cancer and/or the susceptibility to
 CC pancreatic cancer. A compound (antibody, an antibody-derivative, an
 CC antibody fragment, a peptide, or an antisense construct) identified by
 CC screening methods using (I) is useful for treatment or prevention of
 CC pancreatic cancer. It is also useful for the preparation of a diagnostic
 CC composition for diagnosing pancreatic cancer or a predisposition for
 CC pancreatic cancer. The current polypeptides were found to be

CC differentially expressed in pancreatic tissue obtained from individuals
 CC suffering from pancreatic cancer as compared to healthy pancreatic
 CC tissue. They have been identified as suitable as markers of pancreatic
 CC cancer for early diagnosis of the disease. This sequence corresponds to a
 CC protein marker of the invention.

XX SQ Sequence 453 AA;

Query Match 51.7%; Score 60; DB 8; Length 453;
 Best Local Similarity 64.7%; Pred. No. 0.38;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPF 17
 | | | | | : | | | | |
 Db 399 KTRWYSMKTKTKIIPF 415

RESULT 36
 ID AAR84551 standard; protein; 454 AA.

XX AC AAR84551;

XX DT 12-JUN-1996 (first entry)

XX DE Partial human fibrinogen gamma-chain.

XX KW Human fibrinogen; gamma-chain; synthetic 3'-end fragment;

XX KW Bluescript II KS+; plasmid; mp19gamma2; expression vector; pREP9;

XX KW variant fibrin chains; unable to self polymerise; fibrinogen;

XX KW surgical sealants; thrombin activation; pure starting material;

XX KW fibrin-derived factors; regulation; angiogenesis; platelet aggregation.

XX OS Homo sapiens.

XX PN WO9529686-A1.

XX PD 09-NOV-1995.

XX PF 02-MAY-1995; 95WO-US005527.

XX PR 02-MAY-1994; 94US-00236979.

XX PA (SQUI) SQUIBB & SONS INC E R.

XX PI Cederholm-Williams SA;

XX DR WPI; 1995-392917/50.

XX DR N-PSDB; AAT05310.

XX PT Variant chains of fibrin unable to self polymerise - are able to react
 PT with fibrinogen, partic. useful in surgical sealants that do not require
 PT activation of thrombin.

XX PS Disclosure; Fig 7; 102pp; English.

XX CC Using the primers AAT05292/93 a 310 bp fragment from a human fibrinogen
 CC gamma-chain cDNA clone was amplified, and digested to allow the N-
 CC terminal and C-terminal portions of the gamma-chain (a partial nucleotide
 CC and amino acid sequence of which is given in AAT05310 and AAR84551,
 CC respectively) to be purified. They were then ligated along with the
 CC synthetic 3'-end fragment AAT05309, and cloned into a mp19 vector to give
 CC mp19gamma2, which encodes a complete gamma-chain. mp19gamma2 was then
 CC subcloned into the expression vector pREP9, which was used in the prodn.
 CC of variant fibrin chains unable to self polymerise. These chains are able
 CC to react with fibrinogen, partic. useful in surgical sealants that do not
 CC require thrombin activation, and are pure starting materials for fibrin-
 CC derived factors that regulate angiogenesis, platelet aggregation, etc

XX SQ Sequence 454 AA;

Query Match 51.7%; Score 60; DB 2; Length 454;
 Best Local Similarity 64.7%; Pred. No. 0.38;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPF 17
 | ||||| : ||| ||
 Db 416 KTRWYSMKTKTKIIPF 432

RESULT 37
 AAY94009
 ID AAY94009 standard; protein; 454 AA.

XX AC AAY94009;
 XX DT 20-OCT-2000 (first entry)
 XX DE Amino acid sequence of the gamma chain of human fibrinogen.
 XX KW Fibrin sealant; fibrin; surgery; bleeding; adhesion; surgical adhesive;
 XX KW angiogenesis; platelet aggregation; gamma-fibrinogen.
 XX OS Homo sapiens.

XX PN US6083902-A.
 XX PD 04-JUL-2000.
 XX PF 03-MAY-1995; 95US-00434099.
 XX PR 02-MAY-1994; 94US-00236979.
 XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX PI Cederholm-Williams SA;

XX DR WPI; 2000-464370/40.
 XX DR N-PSDB; AAA57835.
 XX PT New fibrin sealant containing human fibrin homolog unable to self-
 PT polymerize but forms non-covalent bond with fibrinogen, useful in surgery
 PT for controlling bleeding or adhering tissues to each other.
 XX PS Example; Fig 7; 39pp; English.

XX CC The present sequence represents the gamma chain of human fibrinogen. The
 CC sequence was used to produce a fibrin sealant. The specification
 CC describes a fibrin sealant which contains a human fibrin-homologue. The
 CC sealant comprises a recombinant variant fibrin chain differing from the
 CC naturally occurring gamma-chain by one or more mutations or deletions in
 CC a C-terminal region following a coiled-coil forming region. When
 CC incorporated into a fibrin-homologue, the homologue cannot self-
 CC polymerize but forms non-covalent bonds or polymerize with fibrinogen.
 CC The fibrin sealants are used in surgery to control bleeding or to adhere
 CC two tissues to each other. The recombinant fibrin chains are used may be
 CC used in the preparation of safe and convenient surgical adhesives and
 CC sealants, and as sources of substantially pure starting material for the
 CC production of fibrin-derived factors that regulate angiogenesis, or
 CC platelet aggregation. Fibrin and fibrin homologues may be used as
 CC components of fibrin monomer-based surgical sealants

SQ Sequence 454 AA;

Query Match 51.7%; Score 60; DB 3; Length 454;
 Best Local Similarity 64.7%; Pred. No. 0.38;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPF 17
 | ||||| : ||| ||
 Db 416 KTRWYSMKTKTKIIPF 432

RESULT 38
 ABG62851
 ID ABG62851 standard; peptide; 20 AA.

XX ABG62851;
 XX DT 21-AUG-2002 (first entry)
 XX DE Ligand/receptor specificity domain #41.
 XX KW Ligand/receptor specificity exchanger; antibody; pathogen receptor;
 KW bacterial infection; viral infection; yeast infection; cancer;
 KW parasitic infection; fungal infection; proliferation; antibacterial;
 KW virucide; cytostatic; antifungal; ligand/receptor specificity domain.
 XX OS Synthetic.
 XX PN WO200224887-A2.
 XX PD 28-MAR-2002.
 XX PF 19-SEP-2001; 2001WO-IB002327.
 XX PR 19-SEP-2000; 2000US-00664025.
 XX PA (TRIP-) TRIPEP AB.
 XX PI Sallberg M, Flock J;
 XX WPI; 2002-489707/52.
 XX Novel ligand/receptor specificity exchanger that redirects antibodies to
 PT receptors on pathogen or tumor cell, has specificity domain having ligand
 PT for receptor, and antigenic domain having epitope of pathogen or toxin.
 XX PS Claim 6; Page 13; 79pp; English.

XX CC The present invention relates to ligand/receptor specificity exchangers
 CC comprising at least one specificity domain comprising a ligand for a
 CC receptor, and at least one antigenic domain joined to the specificity
 CC domain, where the antigenic domain comprises an epitope of a pathogen or
 CC toxin. The ligand/receptor specificity exchangers redirect antibodies to
 CC receptors present on pathogens. They are useful for preventing and
 CC treating human diseases such as bacterial, viral, yeast, parasitic and
 CC fungal infections, and cancer. These compositions act by inhibiting
 CC proliferation of pathogens, or cancer cells. One of the prophylactic
 CC applications of the ligand/receptor specificity exchangers includes
 CC coating or crosslinking it to a medical device or implant which include
 CC implantable medical devices that tend to serve as foci for infection by a
 CC number of bacterial species. ABG62811-ABG62852 represent ligand/receptor
 CC specificity domains used in the methods of the present invention

SQ Sequence 20 AA;

Query Match 50.0%; Score 58; DB 5; Length 20;
 Best Local Similarity 71.4%; Pred. No. 0.029;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
 | ||||| : ||| ||
 Db 2 WYSMRKTKTKIIPF 15

RESULT 39
 ADM73982
 ID ADM73982 standard; peptide; 20 AA.

XX AC ADM73982;
 XX DT 03-JUN-2004 (first entry)

DE Ligand/receptor specificity exchanger specificity domain seqid 41.

XX cytostatic; antifungal; virucide; antibacterial; antiparasitic;
 KW gene therapy; ligand specificity exchanger; specificity domain;
 KW bacterial receptor ligand; antigenic domain; cancer; infection; cancer;

KW receptor specificity exchanger.

OS Synthetic.

PN US2003225251-A1.

XX 04-DEC-2003.

XX 21-FEB-2003; 2003US-00372735.

XX 27-APR-1995; 95WO-SE000468.

XX 27-DEC-1996; 96US-00737085.

XX 08-FEB-1999; 99US-00246258.

XX 21-MAR-2000; 2000US-00532106.

XX 21-APR-2000; 2000US-00556605.

XX 19-SEP-2000; 2000US-00664025.

XX 19-SEP-2000; 2000US-00664945.

XX 19-APR-2001; 2001US-00839666.

XX 20-APR-2001; 2001US-00839447.

XX 19-SEP-2001; 2001WO-IB002327.

XX 21-MAY-2002; 2002US-00153271.

XX 30-AUG-2002; 2002US-00234579.

XX (SALL/) SALLBERG M.

FA (FLOC/) FLOCK J.

XX Sallberg M, Flock J;

XX WPI; 2004-022083/02.

XX New ligand specificity exchanger comprising specificity or antigenic

PT domain, useful in preparing a composition for treating e.g., cancer or

PT infections caused by virus, bacteria, parasite, fungus or yeast.

XX Disclosure; SEQ ID NO 41; 65pp; English.

XX The invention describes a new ligand specificity exchanger comprising a

CC specificity domain comprising a ligand for a bacterial receptor and an

CC antigenic domain joined to the specificity domain and comprising at least

CC 5 and less than 200 consecutive amino acids of a protein from a pathogen

CC or toxin. The ligand specificity exchanger is useful in preparing a

CC composition for treating e.g., cancer or infections caused by virus,

CC bacteria, parasite, fungus or yeast by redirecting existing antibodies to

CC pathogens and cancer cells. This is the amino acid sequence of a

CC ligand/receptor specificity exchanger specificity domain.

XX Sequence 20 AA;

SQ Query Match 50.0%; Score 58; DB 8; Length 20;

Best Local Similarity 71.4%; Pred. No. 0.029;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17

Db 2 WYSMKTKTKIIPF 15

RESULT 40

ABG62912

ID ABG62912 standard; peptide; 27 AA.

XX ABG62912;

XX 21-AUG-2002 (first entry)

XX Ligand/receptor specificity exchanger peptide #43.

XX Ligand/receptor specificity exchanger; antibody; pathogen receptor;

XX bacterial infection; viral infection; yeast infection; cancer;

XX parasitic infection; fungal infection; proliferation; antibacterial;

XX virucide; cytostatic; antifungal.

XX Herpes simplex virus.

OS Synthetic.

PN WO200224887-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-IB002327.

XX 19-SEP-2000; 2000US-00664025.

XX (TRIP-) TRIPEP AB.

XX Sallberg M, Flock J;

XX WPI; 2002-489707/52.

XX Novel ligand/receptor specificity exchanger that redirects antibodies to

PT receptors on pathogen or tumor cell, has specificity domain having ligand

PT for receptor, and antigenic domain having epitope of pathogen or toxin.

XX Claim 19; Page 24; 79pp; English.

XX The present invention relates to ligand/receptor specificity exchangers

CC comprising at least one specificity domain comprising a ligand for a

CC receptor, and at least one antigenic domain joined to the specificity

CC domain, where the antigenic domain comprises an epitope of a pathogen or

CC toxin. The ligand/receptor specificity exchangers redirect antibodies to

CC receptors present on pathogens. They are useful for preventing and

CC treating human diseases such as bacterial, viral, yeast, parasitic and

CC fungal infections, and cancer. These compositions act by inhibiting

CC proliferation of pathogens, or cancer cells. One of the prophylactic

CC applications of the ligand/receptor specificity exchangers includes

CC coating or crosslinking it to a medical device or implant which include

CC implantable medical devices that tend to serve as foci for infection by a

CC number of bacterial species. ABG62870-ABG62915 and ABG62945-ABG62954

CC represent ligand/receptor specificity exchanger peptides used in the

CC methods of the present invention

XX Sequence 27 AA;

SQ Query Match 50.0%; Score 58; DB 5; Length 27;

Best Local Similarity 71.4%; Pred. No. 0.04;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17

Db 2 WYSMKTKTKIIPF 15

RESULT 41

ADM74055

ID ADM74055 standard; peptide; 27 AA.

XX ADM74055;

XX 03-JUN-2004 (first entry)

XX Ligand/receptor specificity exchanger seqid 114.

XX cytostatic; antifungal; virucide; antibacterial; antiparasitic;

XX gene therapy; ligand specificity exchanger; specificity domain;

XX bacterial receptor ligand; antigenic domain; cancer; infection; cancer;

XX receptor specificity exchanger.

XX Synthetic.

XX US2003225251-A1.

XX 04-DEC-2003.

XX 21-FEB-2003; 2003US-00372735.

XX 27-APR-1995; 95WO-SE000468.

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PR 27-DEC-1996; 96US-00737085.
PR 08-FEB-1999; 99US-00246258.
PR 21-MAR-2000; 2000US-00532106.
PR 21-APR-2000; 2000US-00556605.
PR 19-SEP-2000; 2000US-00664025.
PR 19-SEP-2000; 2000US-00664945.
PR 19-APR-2001; 2001US-00839666.
PR 20-APR-2001; 2001US-00839447.
PR 19-SEP-2001; 2001US-00802327.
PR 21-MAY-2002; 2002US-00153271.
PR 30-AUG-2002; 2002US-00234579.
XX
PA (SALL/) SALLBERG M.
PA (FLOC/) FLOCK J.
XX
PI Sallberg M, Flock J;
XX
XX WPI; 2004-022083/02.
XX
XX New ligand specificity exchanger comprising specificity or antigenic
PT domain, useful in preparing a composition for treating e.g., cancer or
PT infections caused by virus, bacteria, parasite, fungus or yeast.
XX
XX Example 7; SEQ ID NO 114; 65pp; English.
XX
XX The invention describes a new ligand specificity exchanger comprising a
CC specificity domain comprising a ligand for a bacterial receptor and an
CC antigenic domain joined to the specificity domain and comprising at least
CC 5 and less than 200 consecutive amino acids of a protein from a pathogen
CC or toxin. The ligand specificity exchanger is useful in preparing a
CC composition for treating e.g., cancer or infections caused by virus,
CC bacteria, parasite, fungus or yeast by redirecting existing antibodies to
CC pathogens and cancer cells. This is the amino acid sequence of a
CC ligand/receptor specificity exchanger of the invention.
XX
SQ Sequence 27 AA;

Query Match 50.0%; Score 58; DB 8; Length 27;
Best Local Similarity 71.4%; Pred. No. 0.04;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
   ||||:|||||
Db 2 WYSMKTKTKIIPF 15

RESULT 42
AAP40614
ID AAP40614 standard; peptide; 38 AA.
XX
XX AAP40614;
AC
XX
DT 16-AUG-2002 (revised)
DT 04-FEB-1992 (first entry)
XX
DE Sequence of peptide inhibitor (PI) obtd. as a plasmin degradation prod.
DE of fragment Di of fibrinogen.
XX
XX Anticoagulant; blood clotting inhibitor; fibrin-binding;
XX thrombus imaging agent.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 32..38
FT /note= "specifically claimed"
FT Misc-difference 33..38
FT /note= "specifically claimed"
FT Misc-difference 34..38
FT /note= "specifically claimed"
XX
XX US4455290-A.
XX

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PD 19-JUN-1984.
XX
XX 02-APR-1981; 81US-00250173.
XX
XX 02-APR-1981; 81US-00250173.
XX
XX (RESE ) RESEARCH CORP.
XX
XX Olexa SA, Budzynski AZ;
PI
XX WPI; 1984-170828/27.
XX
XX Peptide(s) isolated from fibrinogen Fragment Di - useful as
PT anticoagulants and as thrombus imaging agents.
XX
XX Claim 4; Col 14; 16pp; English.
XX
XX A peptide with the SQ in AAP40614 is claimed together with peptides which
CC comprise an AA SQ intermediate between residues 1-38 and 34-38 of
CC AAP40614, e.g. see FT. (Updated on 16-AUG-2002 to add missing OS field.)
XX
XX Sequence 38 AA;

Query Match 50.0%; Score 58; DB 1; Length 38;
Best Local Similarity 71.4%; Pred. No. 0.058;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
   ||||:|||||
Db 3 WYSMKTKTKIIPF 16

RESULT 43
AAW57671
ID AAW57671 standard; peptide; 73 AA.
XX
XX AAW57671;
AC
XX
DT 27-AUG-1998 (first entry)
XX
DE Collagen-like polymer.
XX
XX Collagen-like polymer; synthetic polymer; fibre coating;
XX prosthetic device; catalytic substance.
XX
XX Synthetic.
XX
XX US5773249-A.
XX
XX 30-JUN-1998.
XX
XX 02-MAY-1996; 96US-00642255.
XX
XX 04-NOV-1986; 86US-00927258.
XX
XX 29-OCT-1987; 87US-00114618.
XX
XX 09-NOV-1988; 88US-00269429.
XX
XX 06-NOV-1990; 90US-00609716.
XX
XX 12-NOV-1991; 91US-00791960.
XX
XX 05-NOV-1992; 92US-00972032.
XX
XX 22-DEC-1995; 95US-00577046.
XX
XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
XX Ferrari FA, Cappello J;
XX
XX WPI; 1998-387004/33.
XX
XX Recombinant collagen-like polymers - useful for making gels, films,
PT fibres, etc.
XX
XX Example 7; Col 53; 93pp; English.
XX
XX This sequence represents a unnatural collagen-like polymer of the
CC

```

CC invention. The products may be used as films, fibres, moulded objects and
 CC admixed with other natural or synthetic polymers or coatings on fibres,
 CC films, labware or other surfaces, e.g. prosthetic devices. The polymers
 CC may be used for binding a wide variety of specific binding materials, as
 CC catalytic substances (where the amino acid sequence may specifically
 CC chelate a wide variety of elements), as purification media, composites,
 CC laminates or adhesives. They may also be combined with inorganic or
 CC organic materials such as carbon fibres, nylon fibres, nitrocellulose,
 CC etc., as flask coatings or in synthetic matrices for the growth and study
 CC of cells, as affinity columns or as supports for biological materials.
 CC The polymers have collagen-like properties, but may be easily expressed
 CC in micro-organisms in high efficiency. The new sequences can be tailored
 CC to give the desired properties

XX SQ Sequence 73 AA;

Query Match 50.0%; Score 58; DB 2; Length 73;
 Best Local Similarity 71.4%; Pred. No. 0.12; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2;

Qy 4 WYSMRKMSMKIRPF 17
 |||||:|||||
 Db 35 WYSMKTTMKIIPF 48

RESULT 44
 AAR80332
 ID AAR80332 standard; protein; 75 AA.

XX AC AAR80332;

XX DT 18-APR-1996 (first entry)

XX DE Protein polymer adhesion substrate 1-D monomeric repeat unit.

XX KW Pendant group; repeating unit; enzyme recognition site; sealant; fibrin;
 XX KW enzymatic cross-linking; biocompatible material; structural integrity;
 XX KW medical adhesive; wound closure; tissue repair; transglutaminase.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Domain 33..53
 XX FT /note= "human fibrin POLSITE"
 XX FT Domain 54..73
 XX FT /note= "human fibrin-derived peptide 93.4"

XX EN W09523611-A1.

XX PD 08-SEP-1995.

XX PF 03-MAR-1995; 95WO-US002728.

XX PR 03-MAR-1994; 94US-00205518.

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX PI Cappello J;

XX DR WPI; 1995-320413/41.

XX DR N-PSDB; AAQ98715.

XX FT Protein polymers comprising repeating units and sequences - capable of
 XX FT enzyme-catalysed covalent bond formation useful as a biocompatible
 XX FT material for wound closure and tissue repair.

XX PS Example 4; Page 48; 138pp; English.

XX CC The amino acid sequence of the protein polymer adhesion substrate (PPAS)
 XX CC 1-D monomer repeat unit. The sequence comprises 2 repeats of the CLP 3.7
 XX CC gene encoded sequence linked to the human fibrin POLSITE sequence and the
 XX CC human fibrin-derived peptide 93.2 (AAR80316; comprising an altered C-
 XX CC terminal 17 amino acid from human fibrin) and used to produce the protein

CC polymer adhesion substrate (PPAS) 1-D (AAR80333). The polymers can be
 CC used in biological systems where in situ formation of a biocompatible
 CC material with structural integrity is required e.g. as medical adhesives
 CC and sealants or for wound closure or tissue repair

XX SQ Sequence 75 AA;

Query Match 50.0%; Score 58; DB 2; Length 75;
 Best Local Similarity 71.4%; Pred. No. 0.12; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2;

Qy 4 WYSMRKMSMKIRPF 17
 |||||:|||||
 Db 35 WYSMKTTMKIIPF 48

RESULT 45

AAW49716
 ID AAW49716 standard; protein; 75 AA.

XX AC AAW49716;

XX DT 25-MAR-2003 (revised)

XX DT 12-OCT-1998 (first entry)

XX DE Protein polymer adhesive substrate PPAS1-C monomer.

XX KW Protein polymer adhesive substrate; PPAS1-C; sealant; wound healing;
 XX KW CLP 3.7; collagen; human.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US5773577-A.

XX PD 30-JUN-1998.

XX PF 02-MAR-1995; 95US-00397633.

XX PR 03-MAR-1994; 94US-00205518.

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX PI Cappello J;

XX DR WPI; 1998-387091/33.

XX DR N-PSDB; AAV32071.

XX FT New recombinant protein polymers - containing naturally occurring
 XX FT repetitive units for crosslinking by enzymes, useful as medical adhesives
 XX FT and sealants, depots and matrices.

XX PS Example 4; Col 29; 70pp; English.

XX CC Potein polymer adhesive substrate PPAS1-C monomer comprises human fibrin
 XX CC gamma chain peptide 93.4 (see AAW49709) inserted into a structural
 XX CC backbone of collagen repeat motifs (see AAW49711). A 59 kDa PPAS1-C
 XX CC polymer (see AAW49717) comprising 10 repeats of the monomer has been
 XX CC expressed in Escherichia coli HB101 transformants. Claimed recombinant
 XX CC protein polymers are capable of covalent crosslinking by enzymatic
 XX CC reaction to form products which set quickly and have good adhesive
 XX CC properties and high strength. CLP (collagen like protein) polymers are
 XX CC extremely soluble in water, allowing protein solutions of over 10 wt.% to
 XX CC be formed while maintaining good flow properties. CLP polymers have good
 XX CC adhesion to hydrophilic surfaces and therefore may adhere well to tissue.
 XX CC The fibrin peptide 93.4 inserts of PPAS1-C provide lysine donor sites for
 XX CC Factor XIIIa mediated cross-linking. (Updated on 25-MAR-2003 to correct
 XX CC PF field.)

XX SQ Sequence 75 AA;

Query Match 50.0%; Score 58; DB 2; Length 75;
 Best Local Similarity 71.4%; Pred. No. 0.12;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
 DB 35 WYSMKTTMKIIPF 48

RESULT 46
 AAW49721
 ID AAW49721 standard; protein; 75 AA.
 XX AC AAW49721;
 XX AC
 XX 25-MAR-2003 (revised)
 DT 12-OCT-1998 (first entry)
 XX
 XX Protein polymer adhesive substrate PPAS1-D monomer.
 DE
 XX Protein polymer adhesive substrate; PPAS1-D; sealant; wound healing;
 KW CLP 3.7; collagen; fibrin; human.
 KW
 XX Synthetic.
 OS Homo sapiens.
 XX US5773577-A.
 PN
 XX 30-JUN-1998.
 PD
 XX 02-MAR-1995; 95US-00397633.
 PF
 XX 03-MAR-1994; 94US-00205518.
 PR
 XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PA
 XX Cappelletto J;
 PI
 XX WPI; 1998-387091/33.
 DR N-PSDB; AAV32073.
 DR
 XX New recombinant protein polymers - containing naturally occurring
 PT repetitive units for crosslinking by enzymes, useful as medical adhesives
 PT and sealants, depots and matrices.
 PT
 XX Example 5; Col 31; 70pp; English.
 PS
 XX Protein polymer adhesive substrate PPAS1-D monomer comprises human fibrin
 CC gamma PUSITE inserted into a structural backbone of collagen repeat
 CC motifs (see AAW49711). A PPAS1-D polymer (see AAW49722) has been
 CC expressed in Escherichia coli HB101 transformants. Claimed recombinant
 CC protein polymers are capable of covalent crosslinking by enzymatic
 CC reaction to form products which set quickly and have good adhesive
 CC properties and high strength. CLP (collagen like protein) polymers are
 CC extremely soluble in water, allowing protein solutions of over 10 wt.% to
 CC be formed while maintaining good flow properties. CLP polymers have good
 CC adhesion to hydrophilic surfaces and therefore may adhere well to tissue.
 CC The fibrin PUSITE confers the ability to polymerise adjacent fibrin
 CC molecules through their specific interaction with the N-terminal residues
 CC of the fibrin alpha chain. (Updated on 25-MAR-2003 to correct PF field.)
 XX

QY 4 WYSMRKMSMKIRPF 17
 DB 35 WYSMKTTMKIIPF 48

RESULT 47
 AAR80333
 ID AAR80333 standard; protein; 125 AA.

Query Match 50.0%; Score 58; DB 2; Length 75;
 Best Local Similarity 71.4%; Pred. No. 0.12;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
 DB 35 WYSMKTTMKIIPF 48

RESULT 47
 AAR80333
 ID AAR80333 standard; protein; 125 AA.

XX AAR80333;
 AC
 XX 18-APR-1996 (first entry)
 DT
 XX Protein polymeric adhesion substrate 1-D.
 DE
 XX
 KW Pendant group; repeating unit; enzyme recognition site; sealant; fibrin;
 KW enzymatic cross-linking; biocompatible material; structural integrity;
 KW medical adhesive; wound closure; tissue repair; transglutaminase.
 XX
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 PH 34. .107
 FT Domain
 FT /note= "this sequence may be repeat 2-20 times"
 XX
 XX WO9523611-A1.
 PN
 XX 08-SEP-1995.
 PD
 XX 03-MAR-1995; 95WO-US002728.
 PF
 XX 03-MAR-1994; 94US-00205518.
 PR
 XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PA
 XX Cappelletto J;
 PI
 XX WPI; 1995-320413/41.
 DR
 XX Protein polymers comprising repeating units and sequences - capable of
 PT enzyme-catalysed covalent bond formation useful as a biocompatible
 PT material for wound closure and tissue repair.
 PT
 XX Example 4; Page 49; 138pp; English.
 PS
 XX The amino acid sequence of the protein polymeric adhesion substrate
 CC (PPAS) 1-D. The protein comprises 2-20 repeats of the PPAS1-D monomeric
 CC repeat (AAR80332) which consists of the CLP 3.7 gene encoded sequence
 CC (AAR80321) linked to the human fibrin PUSITE sequence and the human
 CC fibrin cross-linking substrate peptide 93.2 sequence (AAR80316). The
 CC polymers can be used in biological systems where in situ formation of a
 CC biocompatible material with structural integrity is required e.g. as
 CC medical adhesives and sealants or for wound closure or tissue repair
 CC

QY 4 WYSMRKMSMKIRPF 17
 DB 68 WYSMKTTMKIIPF 81

RESULT 48
 AAW57672
 ID AAW57672 standard; peptide; 198 AA.
 XX
 XX AAW57672;
 AC
 XX 27-AUG-1998 (first entry)
 DT
 XX Collagen-like polymer.
 DE
 XX Collagen-like polymer; synthetic polymer; fibre coating;
 KW prosthetic device; catalytic substance.
 KW
 XX Synthetic.
 OS
 XX US5773249-A.
 PN

Query Match 50.0%; Score 58; DB 2; Length 125;
 Best Local Similarity 71.4%; Pred. No. 0.21;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
 DB 68 WYSMKTTMKIIPF 81

RESULT 48
 AAW57672
 ID AAW57672 standard; peptide; 198 AA.
 XX
 XX AAW57672;
 AC
 XX 27-AUG-1998 (first entry)
 DT
 XX Collagen-like polymer.
 DE
 XX Collagen-like polymer; synthetic polymer; fibre coating;
 KW prosthetic device; catalytic substance.
 KW
 XX Synthetic.
 OS
 XX US5773249-A.
 PN

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XX PD 30-JUN-1998.
XX PF
XX PP 02-MAY-1996; 96US-00642255.
XX PR
XX PA 04-NOV-1986; 86US-00927258.
XX PR 29-OCT-1987; 87US-00114618.
XX PR 09-NOV-1988; 88US-00269429.
XX PR 06-NOV-1990; 90US-00609716.
XX PR 12-NOV-1991; 91US-00791960.
XX PR 05-NOV-1992; 92US-00972032.
XX PR 22-DEC-1995; 95US-00577046.
XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX PI Ferrarri FA, Cappello J;
XX DR WPI; 1998-387004/33.
XX PR
XX PT Recombinant collagen-like polymers - useful for making gels, films,
XX PT fibres, etc.
XX PS Example 7; Col 57; 93pp; English.
XX CC This sequence represents a unnatural collagen-like polymer of the
XX CC invention. The products may be used as films, fibres, moulded objects and
XX CC admixed with other natural or synthetic polymers or coatings on fibres,
XX CC films, labware or other surfaces, e.g. prosthetic devices. The polymers
XX CC may be used for binding a wide variety of specific binding materials, as
XX CC catalytic substances (where the amino acid sequence may specifically
XX CC chelate a wide variety of elements), as purification media, composites,
XX CC laminates or adhesives. They may also be combined with inorganic or
XX CC organic materials such as carbon fibres, nylon fibres, nitrocellulose,
XX CC etc., as flask coatings or in synthetic matrices for the growth and study
XX CC of cells, as affinity columns or as supports for biological materials.
XX CC The polymers have collagen-like properties, but may be easily expressed
XX CC in micro-organisms in high efficiency. The new sequences can be tailored
XX CC to give the desired properties
XX SQ Sequence 198 AA;

Query Match 50.0%; Score 58; DB 2; Length 198;
Best Local Similarity 71.4%; Pred. No. 0.34;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17
Db 68 WYSMKKTTMKIIPF 81
|||||:|||||

RESULT 49
AAW49722
ID AAW49722 standard; protein; 198 AA.
XX AC
XX AC AAW49722;
XX DT 25-MAR-2003 (revised)
XX DT 12-OCT-1998 (first entry)
XX DE Protein polymer adhesive substrate PPAS1-D.
XX KW Protein polymer adhesive substrate; PPAS1-D; sealant; wound healing;
XX KW CLP 3.7; collagen; fibrin; human.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Protein 34..179
XX FT /note= "PPAS1-D monomer, repeated 2-20 times"
XX PN US5773577-A.
XX PA

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PD 30-JUN-1998.
XX PF
XX PP 02-MAR-1995; 95US-00397633.
XX PR
XX PA 03-MAR-1994; 94US-00205518.
XX PR (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX PI Cappello J;
XX DR WPI; 1998-387091/33.
XX PR
XX PT New recombinant protein polymers - containing naturally occurring
XX PT repetitive units for crosslinking by enzymes, useful as medical adhesives
XX PT and sealants, depots and matrices.
XX PS Example 5; Col 31; 70pp; English.
XX CC Protein polymer adhesive substrate PPAS1-D comprises multiple repeats of
XX CC a monomer (see AAW49721) consisting of human fibrin POLSITE inserted into
XX CC a structural backbone of collagen repeat motifs (see AAW49711). The PPAS1
XX CC -D polymer has been expressed in Escherichia coli HB101 transformants.
XX CC Claimed recombinant protein polymers are capable of covalent crosslinking
XX CC by enzymatic reaction to form products which set quickly and have good
XX CC adhesive properties and high strength. CLP (collagen like protein)
XX CC polymers are extremely soluble in water, allowing protein solutions of
XX CC over 10 wt.% to be formed while maintaining good flow properties. CLP
XX CC polymers have good adhesion to hydrophilic surfaces and therefore may
XX CC adhere well to tissue. The fibrin POLSITE confers the ability to
XX CC polymerise adjacent fibrin molecules through their specific interaction
XX CC with the N-terminal residues of the fibrin alpha chain. (Updated on 25-
XX CC MAR-2003 to correct PF field.)
XX SQ Sequence 198 AA;

Query Match 50.0%; Score 58; DB 2; Length 198;
Best Local Similarity 71.4%; Pred. No. 0.34;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17
Db 68 WYSMKKTTMKIIPF 81
|||||:|||||

RESULT 50
AAR65759
ID AAR65759 standard; protein; 314 AA.
XX AC
XX AC AAR65759;
XX DT 25-MAR-2003 (revised)
XX DT 17-MAY-1995 (first entry)
XX DE Rat hepatic parenchymal cell growth factor.
XX KW Hepatic parenchymal cell growth factor; HPGF; liver diseases;
XX KW liver cancer; cirrhosis.
XX OS Rattus rattus.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT /label= sig_peptide
XX PN WO9421678-A1.
XX PD 29-SEP-1994.
XX PF 22-MAR-1994; 94WO-JP000455.
XX PR 23-MAR-1993; 93JP-00063905.
XX PA (TAIS ) TAISHO PHARM CO LTD.

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XX Hara H, Yoshimura H, Matsuki Y, Shindo S, Hanada K;
PI WPI; 1994-316940/39.
XX DR N-PSDB; AAQ77818.
XX Hepatic parenchymal cell growth promoter peptide - is isolated from human
PT or animal liver cell or produced by recombinant techniques and used for
PT therapy of liver diseases.
XX Claim 3; Page 34; 47pp; Japanese.
XX AAQ77818 encodes AAR65759 rat hepatic parenchymal cell growth factor
CC (HPGF). The protein or the N-terminal peptide (AAR65758) may be used in
CC the diagnosis and treatment of liver diseases, such as liver cancer and
CC cirrhosis. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 314 AA;
Query Match 50.0%; Score 58; DB 2; Length 314;
Best Local Similarity 52.4%; Pred. No. 0.55;
Matches 11; Conservative 4; Mismatches 4; Indels 2; Gaps 1;
QY 1 KGSWYSMRKMSMKIRP--FFP 19
Db :||||:|||||
291 RGWYSLKSVVMKIRPSDFIP 311

Search completed: January 18, 2005, 11:10:45
Job time : 156 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 11:04:00 ; Search time 39 Seconds

(without alignments)
51.809 Million cell updates/sec

Title: US-09-487-790A-1

Perfect score: 116

Sequence: 1 KGSWYSMRKMSMKIRPFPPQ 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

PIR_79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	100.0	55	2 I67595	beta-fibrinogen -
2	116	100.0	491	1 FGHUB	fibrinogen beta ch
3	106	91.4	328	2 A05229	fibrinogen beta ch
4	103	88.8	468	1 FGBOB	fibrinogen beta ch
5	97	83.6	463	2 A38463	fibrinogen beta ch
6	83	71.6	479	2 A25052	fibrinogen beta ch
7	60	51.7	437	1 FGHUG	fibrinogen gamma-A
8	60	51.7	453	1 FGHUGB	fibrinogen gamma-B
9	56	48.3	312	2 JN0596	fibrinogen-related
10	56	48.3	437	1 FGRTGA	fibrinogen gamma-A
11	56	48.3	444	2 S05313	fibrinogen gamma-A
12	56	48.3	445	1 FGRTGB	fibrinogen gamma-B
13	51	44.0	438	2 A32670	fibrinogen gamma c
14	51	44.0	866	2 D44234	fibrinogen alpha c
15	49	42.2	716	2 G01627	androgen receptor
16	47.5	40.9	128	1 B64420	conserved hypothet
17	47	40.5	125	2 F71003	hypothetical prote
18	46	39.7	115	2 E70562	hypothetical prote
19	46	39.7	841	1 VGBE37	glycoprotein H - h
20	45	38.8	409	2 F75550	probable transposa
21	44.5	38.4	486	2 C75533	probable lipase -
22	44	37.9	399	2 E71188	hypothetical prote
23	44	37.9	408	2 E75452	probable transposa
24	44	37.9	408	2 G75376	probable transposa
25	44	37.9	493	2 JC8027	type 1 angiotensin
26	44	37.9	901	2 T04108	receptor kinase ho
27	43	37.1	310	2 C69218	transcription init
28	43	37.1	490	1 G69282	hypothetical prote
29	43	37.1	598	2 A75531	hypothetical prote

30	43	37.1	2129	2 T27431	hypothetical prote
31	42.5	36.6	75	2 H69993	hypothetical prote
32	42.5	36.6	395	2 C70957	hypothetical prote
33	42.5	36.6	408	2 A56186	cyclin E - African
34	42.5	36.6	2925	2 T00133	RNA-directed RNA p
35	42	36.2	210	2 C97399	probable sigma 54
36	42	36.2	350	2 D71514	probable sulfite r
37	42	36.2	399	2 T42242	hypothetical 44.2K
38	42	36.2	419	2 A86414	hypothetical prote
39	42	36.2	421	2 T52033	19S proteosome sub
40	42	36.2	432	1 FGLMGS	fibrinogen gamma c
41	42	36.2	607	2 F71094	probable aldehyde
42	42	36.2	663	2 T41963	hypothetical prote
43	42	36.2	714	2 T14080	hypothetical prote
44	42	36.2	822	2 AD3232	conjugal transfer
45	42	36.2	1015	2 B83627	probable RND efflu
46	42	36.2	1025	2 A83186	probable RND efflu
47	42	36.2	1648	2 S57163	probable membrane
48	41.5	35.8	1556	2 S59393	probable membrane
49	41	35.3	147	2 B90464	conserved hypothet
50	41	35.3	210	2 S67771	endoplasmic reticu
51	41	35.3	294	2 G64392	heterodisulfide re
52	41	35.3	312	2 AB2063	hypothetical prote
53	41	35.3	330	2 T43475	hypothetical prote
54	41	35.3	362	2 S23471	uroporphyrinogen d
55	41	35.3	383	2 F82871	conserved hypothet
56	41	35.3	401	2 B64598	tetrahydrodipicol
57	41	35.3	451	2 F75131	hypothetical prote
58	41	35.3	460	2 JC5137	beta-glucosidase (
59	41	35.3	481	2 T05270	probable serine/th
60	41	35.3	506	2 AD3338	cobxyric acid synth
61	41	35.3	607	2 B75071	tungsten-containin
62	41	35.3	1772	2 T36105	probable large gly
63	40.5	34.9	732	1 A35655	peptidyl-dipeptida
64	40.5	34.9	1312	1 A34171	tenascin - African
65	40	34.5	77	2 I51647	

ALIGNMENTS

RESULT 1

I67595

beta-fibrinogen - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C/Accession: I67595

R/Sobczak, J.; Lotti, A.

Exp. Cell Res. 169, 47-56, 1987

A>Title: Molecular cloning of mRNA sequences transiently induced during rat liver regen

A/Reference number: I53408; MUID:87134033; PMID:3817019

A/Accession: I67595

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-55 <RES>

A/Cross-references: UNIPROT:P14480; GB:M35602; NID:G204141; PID:AAA41159.1; PID:G20414

C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

F/1-51/Domain: fibrinogen beta/gamma homology (fragment) <FBG>

Query Match 100.0%; Score 116; DB 2; Length 55;

Best Local Similarity 100.0%; Pred. No. 1.1e-11;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPFPPQ 21

Db 35 KGSWYSMRKMSMKIRPFPPQ 55

RESULT 2

FGHUB

fibrinogen beta chain precursor [validated] - human

N/Alternate names: coagulation factor I

N/Contains: fibrinopeptide B

C;Species: Homo sapiens (man)
 C;Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
 C;Accession: B43568; B90469; B90469; A94433; A90437; A94309; G54223; A03121; B37
 R;Chung, D.W.; Harris, J.E.; Davies, E.W.
 Adv. Exp. Med. Biol. 281, 39-48, 1990
 A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
 A;Reference number: A43568; MUID:91344740; PMID:2102623
 A;Accession: B43568
 A;Molecule type: DNA
 A;Residues: 9-191, 'P', 193-491 <CHU>
 A;Cross-references: UNIPROT:P02675
 R;Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davies, E.W.
 Biochemistry 22, 3244-3250, 1983
 A;Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu
 A;Reference number: A90469; MUID:83283433; PMID:6698356
 A;Accession: A90469
 A;Molecule type: DNA
 A;Residues: 1-38 <CHI>
 A;Accession: B90469
 A;Molecule type: mRNA
 A;Residues: 9-191, 'P', 193-491 <CH2>
 A;Cross-references: GB:J00129; NID:g182429; PIDN:AA52429.1; PID:g182430
 R;Huber, P.; Dalmon, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
 Nucleic Acids Res. 15, 1615-1625, 1987
 A;Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
 A;Reference number: 137389; MUID:87146483; PMID:3029722
 A;Accession: 137389
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-38 <HUB>
 A;Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
 R;Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
 In Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
 A;Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
 A;Reference number: A94433
 A;Contents: carbohydrate binding
 A;Accession: A94433
 A;Molecule type: protein
 A;Residues: 31-137, 'QS', 140-144, 'QF', 147-491 <HEN>
 R;Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
 Biochemistry 18, 68-76, 1979
 A;Title: Amino acid sequence of the beta chain of human fibrinogen.
 A;Reference number: A90437; MUID:79124640; PMID:420779
 A;Accession: A90437
 A;Molecule type: protein
 A;Residues: 31-144, 'QF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
 R;Blomback, B.; Hessel, B.; Hogg, D.
 Thromb. Res. 8, 639-658, 1976
 A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
 A;Reference number: A94309; MUID:76225080; PMID:936108
 A;Contents: disulfide bonds
 A;Accession: A94309
 A;Molecule type: protein
 A;Residues: 31-112, 'E', 114-137, 'QS', 140-144, 'QF', 147-148 <BLQ>
 R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A;Title: Identification of proteins associated with apolipoprotein A-I-containing lipoph
 A;Reference number: A54223; MUID:94162201; PMID:8117655
 A;Accession: G54223
 A;Molecule type: protein
 A;Residues: 164-174 <KUN>
 A;Note: identification of tryptic peptides from high-density lipoproteins
 R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
 Ann. N.Y. Acad. Sci. 408, 28-43, 1983
 A;Title: Covalent structure of fibrinogen.
 A;Reference number: A90037; MUID:83284370; PMID:6575689
 A;Contents: annotation; review; disulfide bonds
 R;Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
 Eur. J. Biochem. 77, 595-610, 1977
 A;Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
 A;Reference number: A91249; MUID:77245999; PMID:891553
 A;Contents: annotation; disulfide bonds
 R;Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G

in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottessen, M., Fol
 A;Title: The structures of fibrinogen and fibrin.
 A;Reference number: A94437
 A;Contents: annotation; disulfide bonds
 R;Doolittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A;Title: Fibrinogen and fibrin.
 A;Reference number: A90041; MUID:84305751; PMID:6383194
 A;Contents: annotation; review, EM structure, polymerization, ligands
 R;Chung, D.W.; Rixon, M.W.; Que, B.G.; Davies, E.W.
 Ann. N.Y. Acad. Sci. 408, 449-456, 1983
 A;Title: Cloning of fibrinogen genes and their cDNA.
 A;Reference number: A90038; MUID:83254384; PMID:6575700
 A;Contents: annotation
 R;Kirschbaum, N.E.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13669-13676, 1990
 A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-t
 A;Reference number: A37117; MUID:90337977; PMID:2143188
 A;Contents: annotation; hementin cleavage site
 A;Note: hementin, a protease from Haemoteria ghiliani, the giant South American leech
 C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleav
 ization sites responsible for the formation of the soft clot.
 C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
 ger) and between alpha chains (weaker) of different monomers.
 C;Comment: All fibrinogen chains are synthesized in the liver.
 C;Genetics:
 A;Gene: GDB:FGB
 A;Cross-references: GDB:119130; OMIM:134830
 A;Map position: 4q28-4q28
 A;Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
 C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:F
 ins are contained in the core. Two three-chain coiled coils emerge from this core and c
 from the distal domain nodes.
 C;Function:
 A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A;Pathway: blood coagulation
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
 C;Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutamic a
 F;1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
 F;31-491/Product: fibrinogen beta chain #status experimental <WAT>
 F;31-44/Product: fibrinopeptide B #status experimental <APT>
 F;45-491/Product: fibrin beta chain #status experimental <FGB>
 F;45-47/Region: polymerization site
 F;99-228/Domain: fibrinogen disulfide ring homology <FDR>
 F;238-487/Domain: fibrinogen beta/gamma homology <FGB>
 F;31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
 F;44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
 F;95/Disulfide bonds: interchain (to alpha-55) #status experimental
 F;106/Disulfide bonds: interchain (to alpha-68) #status experimental
 F;110/Disulfide bonds: interchain (to gamma-45) #status experimental
 F;223/Disulfide bonds: interchain (to alpha-184) #status experimental
 F;227/Disulfide bonds: interchain (to gamma-161) #status experimental
 F;231-316,241-270,424-437/Disulfide bonds: #status experimental
 F;394/Binding site: carbonyl (Asn) (covalent) #status experimental
 Query Match 100.0%; Score 116; DB 1; Length 491;
 Best Local Similarity 100.0%; Pred. No. 9.9e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGSWYSMRKMSKIRPFPPQ 21
 |||||
 Db 471 KGSWYSMRKMSKIRPFPPQ 491
 |||||
 RESULT 3
 A05299
 fibrinogen beta chain precursor - rat (fragments)
 N;Contains: fibrinopeptide B
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 05-Jun-1987 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
 C;Accession: A05299; PF0010
 R;Fowlkes, D.M.; Mullis, N.T.; Comeau, C.M.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 81, 2313-2316, 1984

A;Title: Potential basis for regulation of the coordinately expressed fibrinogen genes:
 A;Reference number: A93989; MUID:84194000; PMID:6232608
 A;Accession: A05299
 A;Molecule type: DNA
 A;Residues: 1-32 <F0W>
 A;Cross-references: UNIPROT:P14480
 R;Eastman, E.M.; Gilula, N.B.
 Gene 79, 151-158, 1989
 A;Title: Cloning and characterization of a cDNA for the B beta chain of rat fibrinogen:
 A;Reference number: PE0010; MUID:89378771; PMID:2673932
 A;Accession: PE0010
 A;Molecule type: mRNA
 A;Residues: 33-328 <AS>
 A;Cross-references: GB:M27220; NID:G529585; PIDN:AAA41160.1; PID:G529586
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 C;Keywords: blood coagulation; glycoprotein; liver; plasma
 F;33-65/Domain: fibrinogen disulfide ring homology (fragment) <FDR>
 F;75-324/Domain: fibrinogen beta/gamma homology <FBG>
 F;231/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.4%; Score 106; DB 2; Length 328;
 Best Local Similarity 90.5%; Pred. No. 2.7e-09;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPFPPQQ 21
 |||||:|||||:|||||
 Db 308 KGSWYSMRKMSMKIRPFPPQQ 328

RESULT 4

FGBOB
 N;Contains: fibrinogen beta chain - bovine
 N;Contains: fibrinopeptide B
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
 C;Accession: A03122; B03117; B37507; A37513; S02443
 R;Blomback, B.; Doolittle, R.F.
 Acta Chem. Scand. 17, 1816-1819, 1963
 A;Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
 A;Reference number: A03122
 A;Accession: A03122
 A;Molecule type: protein
 A;Residues: 1-4 <BLO>
 R;Sjoquist, J.; Blomback, B.; Wallen, P.
 Ark. Kem 16, 425-436, 1960
 A;Title: Amino acid sequence of bovine fibrinopeptides.
 A;Reference number: A03117
 A;Accession: B03117
 A;Molecule type: protein
 A;Residues: 5-21 <SJO>
 R;Martinielli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A;Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
 A;Reference number: A37507; MUID:79164394; PMID:434821
 A;Accession: B37507
 A;Molecule type: protein
 A;Residues: 22-53 <MAR>
 R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
 A;Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
 A;Reference number: A37513; MUID:81199473; PMID:6262803
 A;Accession: A37513
 A;Molecule type: mRNA
 A;Residues: 44-468 <CHU>
 R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
 FEBS Lett. 232, 56-60, 1988
 A;Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
 A;Reference number: S02443; MUID:88211875; PMID:2966748
 A;Accession: S02443
 A;Molecule type: protein
 A;Residues: 373-374 <MED>
 C;Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
 C;Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alp

C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 C;Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein
 F;76-205/Domain: fibrinogen disulfide ring homology <FDR>
 F;215-464/Domain: fibrinogen beta/gamma homology <FBG>
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
 F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
 F;371/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 88.8%; Score 103; DB 1; Length 468;
 Best Local Similarity 81.0%; Pred. No. 1.2e-08;
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPFPPQQ 21
 :|||||:|||||:|||||:|||||
 Db 448 QGSWYSMKMSMKIRPYFPFQ 468

RESULT 5

A38463
 fibrinogen beta chain - chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
 C;Accession: A38463
 R;Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
 Biochemistry 30, 3290-3294, 1991
 A;Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage site
 A;Reference number: A38463; MUID:91182745; PMID:2009266
 A;Accession: A38463
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-463 <WEI>
 A;Cross-references: UNIPROT:Q02020; GB:M58514; NID:g211779; PIDN:AAA48770.1; PID:g211778
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 F;73-202/Domain: fibrinogen disulfide ring homology <FDR>
 F;212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 83.6%; Score 97; DB 2; Length 463;
 Best Local Similarity 84.2%; Pred. No. 1.1e-07;
 Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPFPP 19
 |||||:|||||:|||||:|||||
 Db 444 KGSWYSMKMSMKIKPYFP 462

RESULT 6

A25052
 fibrinogen beta chain - sea lamprey (fragments)
 N;Contains: fibrinopeptide B
 C;Species: Petromyzon marinus (sea lamprey)
 C;Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
 C;Accession: A25052; A03124; B03124
 R;Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
 Biochemistry 25, 6512-6516, 1986
 A;Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
 A;Reference number: A25052; MUID:87076582; PMID:3790537
 A;Accession: A25052
 A;Molecule type: mRNA
 A;Residues: 39-479 <BOH>
 A;Cross-references: UNIPROT:P02678; GB:M14773; NID:g213191; PIDN:AAA49261.1; PID:g21319
 R;Cottrell, B.A.; Doolittle, R.F.
 Biochim. Biophys. Acta 453, 426-438, 1976
 A;Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization o
 A;Reference number: A03120; MUID:77065679; PMID:999898
 A;Accession: A03124
 A;Molecule type: protein
 A;Residues: 1-36 <COT1>
 A;Accession: B03124
 A;Molecule type: protein
 A;Residues: 37-42 <COT2>

C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

A;Gene: GDB:FGG
A;Cross-references: GDB:119132; OMIM:134850
A;Map position: 4q28-4q28
A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGG) and two sets of beta (see PIR:FBG) chains. Two three-chain coiled coils emerge from this core and coil from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into fibrin.
A;Pathway: blood coagulation
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C;Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein.
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-437/Product: fibrinogen gamma-A chain #status experimental <MPT>
F;176-415/Domain: fibrinogen beta/gamma homology <FBG>
F;341-355/Domain: calcium binding #status predicted <CAB>
F;400-422/Region: polymerization site, binding to the amino end of the alpha chain of actin.
F;423-437/Region: platelet aggregation #status predicted
F;34/Disulfide bonds: interchain (to gamma-35) #status experimental
F;35/Disulfide bonds: interchain (to gamma-34) #status experimental
F;45/Disulfide bonds: interchain (to beta-110) #status experimental
F;49/Disulfide bonds: interchain (to alpha-64) #status experimental
F;78/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;161/Disulfide bonds: interchain (to beta-227) #status experimental
F;165/Disulfide bonds: interchain (to alpha-180) #status experimental
F;179-208,352-365/Disulfide bonds: #status experimental
F;424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status experimental
F;432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status experimental

Query Match 51.7%; Score 60; DB 1; Length 437;
Best Local Similarity 64.7%; Pred. No. 0.087;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKSMKIRPF 17
Db 399 KTRWYSMKTKTKIIPF 415

RESULT 8
FGHUGB
N;Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
C;Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R;Xion, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A;Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A;Reference number: A90494; MUID:85252774; PMID:2990550
A;Accession: A90494
A;Molecule type: DNA
A;Residues: 1-113, 'I', 115-453 <RIX>
A;Cross-references: UNIPROT:P02679; GB:M10014; GB:J00135; GB:X00086; NID:g182
R;Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A;Title: Structure of the human gamma-chain-fibrinogen gene. Alternate mRNA splicing near the 5' end.
A;Reference number: A92448; MUID:85030379; PMID:6092346
A;Accession: A92448
A;Molecule type: DNA
A;Residues: 286-453 <FOR>
R;Wolfenstein-Todel, C.; Mossessan, M.W.
Biochemistry 20, 6146-6149, 1981
A;Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant.
A;Reference number: A90453; MUID:82068993; PMID:7306501
A;Accession: A90453
A;Molecule type: protein
A;Residues: 411-434, 'Y', 436-440, 'Z', 442, 'Z', 444, 'B', 446-447, 'R', 449, 'ZBB', 453 <WOL>
R;Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3359-3362, 1988
A;Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain of human fibrinogen.
A;Reference number: A94194; MUID:88217900; PMID:3368448
A;Accession: A28203
A;Molecule type: protein

A;Residues: 433-449 <FRA>
A;Accession: B28203
A;Molecule type: protein
A;Residues: 433-453 <FR2>
R;Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A;Title: Polymorphism of the human gamma chain fibrinogen gene.
A;Reference number: I37390; MUID:92119334; PMID:1685103
A;Accession: I37390
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 75-286 <RES>
A;Cross-references: EMBL:X51473; NID:g31410; PIDN:CAA35837.1; PID:g930064
C;Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate splicing of the gamma chain. The gamma-B chain is present in about 10% of the fibrinogen molecules in plasma.
C;Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plasma.
C;Genetics:
A;Gene: GDB:FGG
A;Cross-references: GDB:119132; OMIM:134850
A;Map position: 4q28-4q28
A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGG) and two sets of beta (see PIR:FBG) chains. Two three-chain coiled coils emerge from this core and coil from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into fibrin.
A;Pathway: blood coagulation
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C;Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein.
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-453/Product: fibrinogen gamma-B chain #status experimental <MPT>
F;176-415/Domain: fibrinogen beta/gamma homology <FBG>
F;341-355/Domain: calcium binding #status predicted <CAB>
F;400-422/Region: polymerization site, binding to the amino end of the alpha chain of actin.
F;34/Disulfide bonds: interchain (to gamma-35) #status predicted
F;35/Disulfide bonds: interchain (to gamma-34) #status predicted
F;45/Disulfide bonds: interchain (to beta-110) #status predicted
F;49/Disulfide bonds: interchain (to alpha-64) #status predicted
F;78/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;161/Disulfide bonds: interchain (to beta-227) #status predicted
F;165/Disulfide bonds: interchain (to alpha-180) #status predicted
F;179-208,352-365/Disulfide bonds: #status predicted
F;424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status predicted
F;432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted

Query Match 51.7%; Score 60; DB 1; Length 453;
Best Local Similarity 64.7%; Pred. No. 0.09;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKSMKIRPF 17
Db 399 KTRWYSMKTKTKIIPF 415

RESULT 9
JN0596
fibrinogen-related protein HFRP-1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text change 09-Jul-2004
C;Accession: JN0596
R;Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A;Title: Molecular cloning and initial characterization of a novel fibrinogen-related protein HFRP-1.
A;Reference number: JN0596; MUID:93290661; PMID:8390249
A;Accession: JN0596
A;Molecule type: mRNA
A;Residues: 1-312 <YAM>
A;Cross-references: UNIPROT:Q08830; GB:D14446; NID:g9393314; PIDN:BAA03336.1; PID:g939331
A;Experimental source: liver
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-312/Product: fibrinogen-related protein HFRP-1 #status predicted <MAT>
F;80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 48.3%; Score 56; DB 2; Length 312;
 Best Local Similarity 55.0%; Pred. No. 0.27;
 Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKSMKIRP--FFP 19
 | | | | : : | | | | |
 Db 290 GWYSLKSVVMKIRPNDIFP 309

RESULT 10
 FGRTGA
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
 C;Accession: A90828; A93989; A03127
 R;Crabtree, G.R.; Kant, J.A.
 Cell 31, 159-166, 1982

A;Title: Organization of the rat gamma-fibrinogen gene: alternative mRNA splice patterns
 A;Reference number: A90828; MUID:83129318; PMID:6897622
 A;Accession: A90828
 A;Molecule type: mRNA
 A;Residues: 1-437 <CRA>
 A;Cross-references: UNIPROT:P02680
 R;Fowlkes, D.M.; Mullis, N.T.; Comeau, C.M.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 81, 2313-2316, 1984
 A;Title: Potential basis for regulation of the coordinately expressed fibrinogen genes:
 A;Reference number: A93989; MUID:84194000; PMID:6232608
 A;Accession: A93989
 A;Molecule type: DNA
 A;Residues: 1-102 <FOW>
 A;Cross-references: GB:K01337; NID:G204102; PIDN:AAA98626.1; PID:G204103
 C;Comment: The fibrinogen molecule is a hexamer containing two sets of three nonidentical

C;Genetics:
 A;Introns: 25/3; 41/3
 C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 C;Keywords: alternative splicing; blood coagulation; plasma
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-437/Product: fibrinogen gamma-A chain #status predicted <FGA>
 F;176-415/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 48.3%; Score 56; DB 1; Length 437;
 Best Local Similarity 58.8%; Pred. No. 0.38;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKSMKIRPF 17
 | | | | : : | | | | |
 Db 399 KTRWYSMKETTKIIPF 415

RESULT 11
 S05313
 fibrinogen gamma-B chain precursor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C;Accession: S05313
 R;Brown, W.M.; Diegilewska, K.M.; Foreman, R.C.; Saunders, N.R.
 Nucleic Acids Res. 17, 6397, 1989
 A;Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrin
 A;Reference number: S05313; MUID:89366676; PMID:2771651
 A;Accession: S05313
 A;Molecule type: mRNA
 A;Residues: 1-444 <PRO>
 A;Cross-references: UNIPROT:P12799; EMBL:X15556; NID:G349; PIDN:CAA33562.1; PID:G350
 A;Note: the authors translated the codon AGT for residue 105 as Ala and ART for residue
 C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
 F;174-414/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 48.3%; Score 56; DB 2; Length 444;
 Best Local Similarity 62.5%; Pred. No. 0.39;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKSMKIRP 16
 | | | | : : | | | | |
 Db 398 KSRWYSMKETTKIIP 413

RESULT 12
 FGRTGB
 fibrinogen gamma-B chain precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 27-Feb-1997
 C;Accession: A03128; I58265
 R;Crabtree, G.R.; Kant, J.A.
 Cell 31, 159-166, 1982

A;Title: Organization of the rat gamma-fibrinogen gene: alternative mRNA splice patterns
 A;Reference number: A90828; MUID:83129318; PMID:6897622
 A;Accession: A03128
 A;Molecule type: mRNA
 A;Residues: 1-445 <CRA>
 R;Morgan, J.G.; Holbrook, N.J.; Crabtree, G.R.
 Nucleic Acids Res. 15, 2774-2776, 1987

A;Title: Nucleotide sequence of the gamma chain gene of rat fibrinogen: conserved intron
 A;Reference number: I58265; MUID:87174801; PMID:3562236
 A;Accession: I58265
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-134 <RES>
 A;Cross-references: EMBL:X05850; NID:G56147; PID:G56148
 C;Comment: Gamma-B is formed from the same gene as gamma-A, probably as a result of fai
 C;Comment: The fibrinogen molecule is a hexamer containing two sets of three nonidentical
 C;Genetics:
 A;Introns: 25/3; 41/3; 103/1
 C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 C;Keywords: alternative splicing; blood coagulation; plasma

F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-445/Product: fibrinogen gamma-B chain #status predicted <FGB>
 F;176-415/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 48.3%; Score 56; DB 1; Length 445;
 Best Local Similarity 58.8%; Pred. No. 0.39;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKSMKIRPF 17
 | | | | : : | | | | |
 Db 399 KTRWYSMKETTKIIPF 415

RESULT 13
 A32670
 fibrinogen gamma chain - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 13-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
 C;Accession: A32670; I51416
 R;Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
 Biochemistry 29, 2599-2605, 1990
 A;Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
 A;Reference number: A32670; MUID:90241882; PMID:2334684
 A;Accession: A32670
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-438 <PAS>
 A;Cross-references: UNIPROT:P17634; GB:J02894; NID:G214139; PIDN:AAA49709.1; PID:G214141
 R;Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
 Mol. Cell. Endocrinol. 72, 213-220, 1990
 A;Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus
 A;Reference number: I51416; MUID:91146806; PMID:2289632
 A;Accession: I51416
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-58 <BHA>

A;Cross-references: GB:M35548; NID:G214141; PIDN:AAA03247.1; PID:G214142
 C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 C;Keywords: blood coagulation
 F;173-413/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 44.0%; Score 51; DB 2; Length 438;
Best Local Similarity 61.5%; Pred. No. 2.4;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSNRKMSMKIRP 16
|||||: :||| |
Db 400 WYSKSVTKIMP 412

RESULT 14
D44234
fibrinogen alpha chain precursor, extended splice form - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: D44234; B44234
R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: D44234
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA; DNA
A;Residues: 1-866 <FU>
A;Cross-references: UNIPROT:P02671; GB:M58569; NID:G182406; PID:G182407
A;Note: neither the complete nucleic acid sequence nor the complete translation are shown
A;Accession: B44234
A;Molecule type: mRNA; DNA
A;Residues: 605-866 <FU2>
A;Note: sequence extracted from NCBI backbone (NCBIP:119917)
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentical
ntained in the core. Two three-chain coiled coils emerge from this core and connect it to
distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
C;Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F;20-863/Product: fibrinopeptide A #status experimental <APT>
F;36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F;57-195/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;629-863/Domain: fibrinogen beta/gamma homology <FBG>
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental
F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status exp

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F:686,831/Binding site: carbohydrate (Asn) #status predicted

Query Match          44.0%; Score 51; DB 2; Length 866;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPFPPQ 20
   |||:|:|:|:|
Db 847 RGADYSLRVVRMKIRPLVTQ 866

RESULT 15
G01627
N/Androgen receptor 1 - human
N/Alternate names: dihydrotestosterone receptor
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C/Accession: G01627
R;Bina, M.
submitted to the EMBL Data Library, December 1994
A/Reference number: G07955
A/Accession: G01627
A/Status: preliminary; translated from GB/EMBL/DBDB
A/Molecule type: mRNA
A/Residues: 1-716 <BIN>
A/Cross-references: EMBL:U19345; NID:g726041; PID:g726042
C/Genetics:
A/Gene: GDB:AR; DHTR; SEMA
A/Cross-references: GDB:l20556; OMIM:313700
A/Map position: Xq11-Xq12

Query Match          42.2%; Score 49; DB 2; Length 716;
Best Local Similarity 47.4%; Pred. No. 8.4;
Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GSWYSMRKMSMKIRPFPPQ 20
   |||:|:|:|:|
Db 545 GKWASVRRNMGDLFGPFYPO 563

RESULT 16
B64420
conserved hypothetical protein MJ0962 - Methanococcus jannaschii
C/Species: Methanococcus jannaschii
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: B64420
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weisscock, K.G.; Merrick, J.M.; Glodek, A
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A/Reference number: A64300; MUID:96337999; PMID:8688087
A/Accession: B64420
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-128 <BUL>
A/Cross-references: UNIPROT:Q58372; GB:U67539; GB:L77117; NID:g1591619; PIDN:AAB98964.1
C/Genetics:
A/Map position: FOR994939-895325
C/Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0962

Query Match          40.9%; Score 47.5; DB 1; Length 128;
Best Local Similarity 35.7%; Pred. No. 2.6;
Matches 10; Conservative 7; Mismatches 4; Indels 7; Gaps 1;

Qy 1 KGSW-----YSMRKMSMKIRPFPPQ 21
   |||:|:|:|:|:|
Db 30 KGNWDRAKRYVYLARIAMQWIRFPKK 57

RESULT 17
F71003

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hypothetical protein PH1324 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: F71003
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71003
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-125 <KAW>
A;Cross-references: UNIPROT:O59042; GB:AP000006; NID:G3236133; PIDN:BAA30430.1; PID:d103
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1324

Query Match 40.5%; Score 47; DB 2; Length 125;
Best Local Similarity 42.1%; Pred. No. 3;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 3 SWYSMRKMSMKIRPFFPQQ 21
|||: : : |||||
Db 101 SWYSISFILTSLVFPFFPIQ 119

RESULT 18
E70562
hypothetical protein Rv3636 - Mycobacterium tuberculosis (strain H37Rv)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E70562
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, K.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70562
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <COL>
A;Cross-references: UNIPROT:O06371; GB:Z95436; GB:AL123456; NID:G3261770; PIDN:CAB08848.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3636

Query Match 39.7%; Score 46; DB 2; Length 115;
Best Local Similarity 44.4%; Pred. No. 4;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 GSWYSMRKMSMKIRPFPFP 19
|||: : : |||||
Db 83 GWYSIRTLSGRVRELRP 100

RESULT 19
VGBE37
glycoprotein H - human herpesvirus 3
N;Alternate names: glycoprotein III
C;Species: human herpesvirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Accession: B27341
R;Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A;Title: The complete DNA sequence of varicella-zoster virus.
A;Reference number: A27345; MUID:86306657; PMID:3018124
A;Accession: B27341
A;Molecule type: DNA
A;Residues: 1-841 <DAV>

A;Cross-references: UNIPROT:P09260; EMBL:X04370; NID:G59989; PIDN:CAA27920.1; PID:G6002.
C;Genetics:
A;Gene: 37
C;Superfamily: herpesvirus glycoprotein H
C;Keywords: glycoprotein
F;18,45,83,217,317,499,522,560,760,783/Binding site: carbohydrate (Asn) (covalent) #sta
Query Match 39.7%; Score 46; DB 1; Length 841;
Best Local Similarity 53.3%; Pred. No. 30;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 YSMRKMSMKIRPFPFP 19
|||: : : |||||
Db 41 YSDRNMSLKLEAFYP 55

RESULT 20
F7550
probable transposase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F7550
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F7550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <WHI>
A;Cross-references: UNIPROT:Q9RXX7; GB:AE001880; GB:AE000513; NID:G6457844; PIDN:AAF097
A;Experimental source: strain R1
C;Genetics:
A;Map position: 1
A;Gene: DR0178
C;Superfamily: hypothetical protein b1432

Query Match 38.8%; Score 45; DB 2; Length 409;
Best Local Similarity 42.1%; Pred. No. 21;
Matches 8; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 1 KGSWYSMRKMSMKIRPFPFP 19
|||: : : |||||
Db 311 KATWYG--RLVSKISPYFP 327

RESULT 21
C75533
probable lipase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: C75533
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75533
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-486 <WHI>
A;Cross-references: UNIPROT:Q9RXX9; GB:AE001893; GB:AE000513; NID:G6458001; PIDN:AAF099
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0334
A;Map position: 1

Query Match 38.4%; Score 44.5; DB 2; Length 486;
Best Local Similarity 27.3%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 7; Indels 13; Gaps 1;

R;Guo, D.F.; Chenier, I.; Tardif, V.; Orlov, S.N.; Inagami, T.
Biochem. Biophys. Res. Commun. 310, 1254-1265, 2003
A;Title: Type 1 angiotensin II receptor-associated protein ARAP1 binds and recycles the
A;Reference number: JC8027; PMID: 14559250
A;Accession: JC8027
A;Molecule type: mRNA
A;Residues: 1-493 <GUO>
A;Cross-references: GB:AF159049
C;Comment: This protein, which interacts with the carboxyl terminal region of the AT1A R
nd specifically promotes the recycling of AT1 receptor back to the plasma membrane after
C;Genetics:
A;Gene: arap1
C;Keywords: angiotensin II receptor; receptor recycling

Query Match 37.9%; Score 44; DB 2; Length 493;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRP 16
: |||::: ||||
Db 472 RGGSYSLKKYVMIRP 487

RESULT 26
T04108
receptor kinase homolog CRINKLY4 - maize
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04108
R;Becraft, P.W.; Stinard, P.S.; McCarty, D.R.
Science 273, 1406-1409, 1996
A;Title: CRINKLY4: A TNFR-like receptor kinase involved in maize epidermal differentiati
A;Reference number: 215216; MUID:96355669; PMID:8703079
A;Accession: T04108
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-901 <BEC>
A;Cross-references: UNIPROT:O24585; EMBL:U67422; NID:gl597722; PIDN:AA809771.1; PID:gl59
A;Experimental source: strain B73
C;Genetics:
A;Gene: cr4
A;Map position: 10S37
C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein

Query Match 37.9%; Score 44; DB 2; Length 901;
Best Local Similarity 56.2%; Pred. No. 67;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRP 16
: |||::: ||||
Db 465 KSTAYSFRKDNMKIQP 480

RESULT 27
C69218
transcription initiation factor TFIIIB - Methanobacterium thermoautotrophicum (strain Del
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69218
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcb
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69218
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-310 <MTH>
A;Cross-references: UNIPROT:O26971; GB:AE000864; GB:AE000666; NID:g2621970; PIDN:AA858
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH885

C;Superfamily: transcription initiation factor IIB; transcription initiation factor IIB
C;Keywords: duplication; transcription initiation
F;13-302/Domain: transcription initiation factor IIB homology <TF2B>

Query Match 37.1%; Score 43; DB 2; Length 310;
Best Local Similarity 46.7%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIR 15
: |||::: ||||
Db 99 RAQWYRLRKWKIR 113

RESULT 28
G69282
hypothetical protein AF0263 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: G69282
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69282
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-490 <KLE>
A;Cross-references: UNIPROT:O29976; GB:AE001087; GB:AE000782; NID:g2689410; PIDN:AA8909
C;Superfamily: Aquifex aeolicus glucose-1-phosphate thymidyltransferase

Query Match 37.1%; Score 43; DB 1; Length 490;
Best Local Similarity 47.4%; Pred. No. 53;
Matches 9; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY 3 SWYSMRKMSMKIRPFPQQ 21
: |||::: ||||
Db 21 NWYSVLKASTAI--FPPEK 37

RESULT 29
A75531
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75531
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75531
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-598 <WHI>
A;Cross-references: UNIPROT:O9RXH6; GB:AE001894; GB:AE000513; NID:g6458011; PIDN:AAF099
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0337
A;Map position: 1

Query Match 37.1%; Score 43; DB 2; Length 598;
Best Local Similarity 41.2%; Pred. No. 64;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPF 17
: |||::: ||||
Db 220 QGAWGQPPRPAPKLRPF 236


```
RESULT 30
T27431
hypothetical protein Y79H2A.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T27431
R/Matthews, L.
submitted to the EMBL Data Library, September 1999
A/Reference number: Z20365
A/Accession: T27431
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2129 <WIL>
A/Cross-references: UNIPROT:Q9U1R8; EMBL:AL110501; NID:e1542357; PIDN:CAB54509.1; CESP:Y
A/Experimental source: clone Y79H2A
C/Genetics:
A/Gene: CESP:Y79H2A.3
A/Introns: 39/3; 75/1; 125/3; 212/3; 254/1; 330/3; 460/1; 486/3; 540/3; 580/3; 631/1; 67
; 1760/1; 1929/3; 2037/3; 2074/3

Query Match 37.1%; Score 43; DB 2; Length 2129;
Best Local Similarity 43.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 YSMRKMGMKIRPPFPQ 20
: : : : :
Db 774 FKLRSENRIFPPFPQ 789

RESULT 31
H6993
hypothetical protein YtjA - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: H6993
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Broutillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: H6993
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-75 <KUN>
A/Cross-references: UNIPROT:Q34601; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB15046.
A/Experimental source: strain 168
C/Genetics:
A/Gene: YtjA
C/Superfamily: conserved hypothetical protein HI1000

Query Match 36.6%; Score 42.5; DB 2; Length 75;
Best Local Similarity 36.8%; Pred. No. 9.5;
Matches 7; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

Qy 1 KGSWYSMRKMGMKIRPPFP 19
: : : : :
Db 45 KGGWLTIKRI-LKCHPFP 62

RESULT 32
C70957
hypothetical protein RV3618 - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: C70957
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: C70957
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-395 <COL>
A/Cross-references: UNIPROT:O07914; GB:Z95557; GB:AL123456; NID:g3242276; PIDN:CAB08948
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV3618
C/Superfamily: alkanal monooxygenase [FMN-linked] (bacterial luciferase)

Query Match 36.6%; Score 42.5; DB 2; Length 395;
Best Local Similarity 30.0%; Pred. No. 51;
Matches 6; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Qy 4 WYSMRKMGMKIRPF---FPQ 20
: : : : :
Db 157 WFTLREAOQLHIRPYTWYP 176

RESULT 33
A56186
cyclin E - African clawed frog
N/Alternate names: Cyclin E1
C/Species: Xenopus laevis (African clawed frog)
C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 12-Jul-2004
C/Accession: A56186; S34125
R/Rempel, R.E.; Sleight, S.B.; Maller, J.L.
J. Biol. Chem. 270, 6843-6855, 1995
A/Title: Maternal Xenopus Cdk2-cyclin E complexes function during meiotic and early emb
A/Reference number: A56186; MUID:95204484; PMID:7896832
A/Accession: A56186
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-408 <REM>
A/Cross-references: UNIPROT:Q91780; GB:L23857; NID:g431745; PIDN:AAA73524.1; PID:g43174
R/Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, June 1992
A/Description: Cloning and expression of Xenopus cyclin E.
A/Reference number: S34125
A/Accession: S34125
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-32, 'A', 34-199, 'NV', 202-258, 'GN', 261-408 <COU>
A/Cross-references: EMBL:Z13966
C/Superfamily: cyclin, A/B/D/E type
C/Keywords: cell cycle control

Query Match 36.6%; Score 42.5; DB 2; Length 408;
Best Local Similarity 30.8%; Pred. No. 53;
Matches 8; Conservative 7; Mismatches 4; Indels 7; Gaps 1;

Qy 3 SWYS-----MRKMGMKIRPPFPQ 21
: : : : :
Db 247 SWNFVFLQVAYIRELQQFLRPFPQ 272

RESULT 34
T00133
RNA-directed RNA polymerase (EC 2.7.7.48) - rice grassy stunt virus
C/Species: rice grassy stunt virus
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T00133
```


R;Staub, J.M.; Kwok, S.F.; Deng, X.W.
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana homologue of human 19S proteasome subunit S9.
A:Reference number: 225911
A:Accession: T52033
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-421 <STA>
A:Cross-references: UNIPROT:O81694; EMBL:AF083890; PIDN:AAC34120.1
C:Superfamily: Caenorhabditis elegans 26S proteasome regulatory complex chain p44.5

Query Match 36.2%; Score 42; DB 2; Length 421;
Best Local Similarity 58.3%; Pred. No. 65;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 MRKSMKIRPFF 18
Db 63 LRKULTKLRPFF 74

RESULT 40
FGLMGS
fibrinogen gamma chain precursor - sea lamprey
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A03129
R:Strong, D.D.; Moore, M.; Cottrell, B.A.; Bohonus, V.L.; Pontes, M.; Evans, B.; Riley, Biochemistry 24, 92-101, 1985
A:Title: Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and general character
A:Reference number: A03129; MUID:85199776; PMID:2581603
A:Accession: A03129
A:Molecule type: mRNA
A:Residues: 1-432 <STR>
A:Cross-references: UNIPROT:P04115; GB:K03049; NID:G213193; PIDN:AAA49262.1; PID:G213194
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation; glycoprotein; liver; plasma; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-432/Product: fibrinogen gamma chain #status experimental <MPT>
F:175-411/Domain: fibrinogen beta/gamma homology <PBG>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F:227/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:421/Cross-link: isopeptide (Gln) (interchain to Lys-425 N6-amino) #status predicted
F:425/Cross-link: isopeptide (Lys) (interchain to Gln-421) #status predicted

Query Match 36.2%; Score 42; DB 1; Length 432;
Best Local Similarity 46.2%; Pred. No. 67;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRP 16
Db 398 WYSLKMTTKLPP 410

RESULT 41
F71094
probable aldehyde ferredoxin oxidoreductase PH1019 [similarity] - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: F71094
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: F71094
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-607 <KAW>
A:Cross-references: UNIPROT:O58778; GB:AP000004; NID:G3236131; PIDN:BA30116.1; PID:G329
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1019

Query Match 36.2%; Score 42; DB 2; Length 607;
Best Local Similarity 36.8%; Pred. No. 95;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 GSWYSMRKMSMKIRPFPQ 20
Db 38 GIVFLLKEMDPKIDPSPPE 56

RESULT 42
T41963
hypothetical protein U60-U66 - human herpesvirus 7 (strain JI)
C:Species: human herpesvirus 7
A:Variety: strain JI
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41963
R;Nicholas, J.
A:Description: Determination and analysis of the complete nucleotide sequence of human
A:Reference number: Z22022
A:Accession: T41963
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-663 <NIC>
A:Cross-references: UNIPROT:P52462; EMBL:U43400; PIDN:AAC54723.1
C:Genetics:
A:Experimental source: strain JI
A:Introns: 288/3
A:Note: U60-U66
C:Superfamily: herpesvirus 38K protein

Query Match 36.2%; Score 42; DB 2; Length 663;
Best Local Similarity 42.1%; Pred. No. 1e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 SWYSMRKMSMKIRPFPQ 21
Db 241 SHFVMDKVEFKRRFPQK 259

RESULT 43
T14080
hypothetical protein F9N11.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14080
R;Bevan, M.; Kalicki, J.; Wohldmann, P.; Smith, A.; Bancroft, I.; Mewes, H.W.; Mayer, K submitted to the Protein Sequence Database, August 1999
A:Reference number: Z17873
A:Accession: T14080
A:Molecule type: DNA
A:Residues: 1-714 <BEV>
A:Cross-references: UNIPROT:Q9SUM4; EMBL:AL109796
A:Experimental source: cultivar Columbia; BAC clone F9N11
C:Genetics:
A:Gene: ATSP:F9N11.50
A:Map position: 4
A:Introns: 7/1; 139/1; 349/1

Query Match 36.2%; Score 42; DB 2; Length 714;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SWYSMRKMSMKIR 15
Db 648 TWYSLRATSOEIR 660

RESULT 44
AD3232
conjugal transfer protein trbE [imported] - Agrobacterium tumefaciens (strain C58, Dupo
C:Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD3232
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3232
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-822 <KUR>
A;Cross-references: UNIPROT:Q9R488; GB:AE008690; PIDN:AAL46274.1; PID:gl7744055; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: trbE
A;Genome: plasmid
C;Superfamily: virB4 protein

Query Match 36.2%; Score 42; DB 2; Length 822;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 8 RKMSMKIRPFPPQ 20
Db 295 KRWQKVRPFPPQ 307

RESULT 45
B83627
Probable RND efflux transporter PA0158 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83627
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83627
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1015 <STO>
A;Cross-references: UNIPROT:Q916X4; GB:AE004453; GB:AE004091; NID:g9945978; PIDN:AAG0354
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0158

Query Match 36.2%; Score 42; DB 2; Length 1015;
Best Local Similarity 47.1%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPFPPQ 20
Db 112 WYQVRKKISDIQGEFPQ 128

RESULT 46
A83186
Probable RND efflux transporter PA3676 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83186
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83186

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1025 <STO>
A;Cross-references: UNIPROT:Q9HXW4; GB:AE004787; GB:AE004091; NID:g9949835; PIDN:AAG070
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3676

Query Match 36.2%; Score 42; DB 2; Length 1025;
Best Local Similarity 47.1%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPFPPQ 20
Db 110 WYQIRKKISDIRATLPQ 126

RESULT 47
S57163
Probable membrane protein YJR140c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J2161
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S57163; S57169
R;Rose, M.; Koetter, P.; Entian, K.D.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56848
A;Accession: S57163
A;Molecule type: DNA
A;Residues: 1-1648 <ROS>
A;Cross-references: UNIPROT:P47171; EMBL:Z49640; NID:gl015881; PID:gl015882; MIPS:YJR14
R;Scarcez, T.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57169
A;Accession: S57169
A;Molecule type: DNA
A;Residues: 1-1647 <SCA>
A;Cross-references: EMBL:Z49640; MIPS:YJR140c
C;Genetics:
A;Gene: SGD:HIR3
A;Cross-references: SGD:S0003901; MIPS:YJR140c
A;Map position: 10R
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YJR140c
C;Keywords: transmembrane protein

Query Match 36.2%; Score 42; DB 2; Length 1648;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 YSMRKMSMKIRP 16
Db 1095 YKMRKSMQARP 1106

RESULT 48
S59393
Probable membrane protein YLR247c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L9672.14
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S59393
R;Johnson, D.
submitted to the EMBL Data Library, February 1995
A;Description: The sequence of S. cerevisiae cosmid 9672.
A;Reference number: S59386
A;Accession: S59393
A;Molecule type: DNA
A;Residues: 1-1556 <JOH>
A;Cross-references: UNIPROT:Q06554; EMBL:U20865; NID:g662330; PID:g662344; GSPDB:GN0001
A;Experimental source: strain S288C (AB972)
C;Genetics:
A;Gene: MIPS:YLR247c
A;Cross-references: SGD:S0004237

```

F;96-112/Domain: transmembrane #status predicted <TM3>
F;141-157/Domain: transmembrane #status predicted <TM4>

Query March          35.3%; Score 41; DB 2; Length 210;
Best Local Similarity 30.0%; Pred. No. 47;
Matches 6; Conservative 8; Mismatches 8; Indels 0; Gaps 0

Qy      2 GSWYSMRKMSMKIRPPFPQ 21
      | | | | : : : | :
Db      156 GLWYSNMDLQKRLKEFYAQE 175

Search completed: January 18, 2005, 11:04:48
Job time : 42 secs

```

A;Map position: 12R
C;Keywords: Transmembrane protein
F;1235-1282;Domain: RING finger homology <RRN>
F;1236-1252;Domain: transmembrane #status predicted <TMM>

Query Match 35.8%; Score 41.5; DB 2; Length 1556;
Best Local Similarity 56.2%; Pred No. 3e+02; 3; Indels 1; Gaps 1;
Matches 9; Conservative 3; Mismatches 3

Qy 5 YSMRXKSMKIRPFPPQ 20
|| :|||:|
Db 268 YSKDRLS-KIKPLPQ 282

RESULT 49
B90464
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: B90464
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Jensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90464
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <KUR>
A;Cross-references: UNIPROT:Q97UX9; GB:AE006641; NID:g13816220; PIDN:AAK42969.1; GSPDB:G
C;Genetics:
A;Gene: SSO2861

```

Query Match          35.3%; Score 41; DB 2; Length 147;
Best Local Similarity 41.2%; Pred.No. 33;
Matches 7; Conservative 6; Mismatches 2; Indels 2; Gaps 1;

Qy      2 GSWYSMR--KWSMKIRP 16
      |||:|||:::||
Db      130 GTWYIIRDKINNVQP 146

RESULT 50
S67771
endoplasmic reticulum membrane protein SHR3 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D1022; protein YDL212W
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67771; S31270
R;Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67756
A;Accession: S67771
A;Molecule type: DNA
A;Residues: 1-210 <SCH>
A;Cross-references: UNIPROT:Q12413; EMBL:Z74260; NID:g1431353; PIDN:CAA98790.1; PID:e253
A;Experimental source: strain S288C
R;Ljungdahl, P.O.; Gimeno, C.J.; Styles, C.A.; Fink, G.R.

```

Ce11 1.7, 403-476, 1952

A:Title: SHR3: a novel component of the secretory pathway specifically required for local

A:Reference number: S31270; MUID:93046646; PMID:1423607

A:Accession: S31270

A:Molecule type: DNA

A:Residues: 1-124,'EKLR', 130-210 <LJU>

A:Cross-references: EMBL:L01264; MID:g172571; PIDN:AAA35035.1; PID:g172572

C:Genetics:

A:Gene: SGD:SHR3

A:Cross-references: SGD:S0002371; MIPS:YDL212w

A:Map position: 4L

C:Keywords: endoplasmic reticulum; transmembrane protein

F:10-26/Domain: transmembrane #status predicted <TM1>

F:62-78/Domain: transmembrane #status predicted <TM2>

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 11:08:15 ; Search time 146 Seconds
(without alignments)
51.966 Million cell updates/sec

Title: US-09-487-790A-1

Perfect score: 116

Sequence: 1 KGSWYSMRKMSKIRPFPPQ 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 65 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	489	9	US-09-989-920-185
2	116	100.0	491	14	US-10-017-724-6
3	113	97.4	488	10	US-09-919-039-33
4	60	51.7	16	16	US-10-181-187D-11
5	60	51.7	20	16	US-10-181-187D-1
6	60	51.7	242	14	US-10-298-461-27
7	60	51.7	437	16	US-10-648-593-171
8	60	51.7	453	17	US-10-733-969A-66
9	58	50.0	20	14	US-10-372-735-41
10	58	50.0	20	15	US-10-608-541-41
11	58	50.0	27	14	US-10-372-735-114
12	58	50.0	27	15	US-10-608-541-102
13	57	49.1	10	16	US-10-181-187D-7

14	57	49.1	411	9	US-09-912-741B-1	Sequence 1, Appli
15	57	49.1	411	9	US-09-912-740A-1	Sequence 1, Appli
16	56	48.3	50	9	US-09-864-761-46553	Sequence 45553, A
17	56	48.3	282	10	US-09-992-600A-28	Sequence 28, Appl
18	56	48.3	282	10	US-09-924-340-28	Sequence 28, Appl
19	56	48.3	282	10	US-09-992-095B-28	Sequence 28, Appl
20	56	48.3	282	10	US-09-999-570-28	Sequence 28, Appl
21	56	48.3	282	14	US-10-000-489-28	Sequence 28, Appl
22	56	48.3	282	14	US-10-000-986-28	Sequence 28, Appl
23	56	48.3	282	14	US-10-000-986-28	Sequence 28, Appl
24	56	48.3	339	9	US-09-925-301-1082	Sequence 1082, Ap
25	52	44.8	217	10	US-09-832-355A-23	Sequence 23, Appl
26	51	44.0	221	13	US-10-112-527-3	Sequence 2, Appli
27	51	44.0	236	13	US-10-112-527-2	Sequence 2, Appli
28	51	44.0	251	13	US-10-112-527-1	Sequence 1, Appli
29	51	44.0	471	15	US-10-282-122A-62157	Sequence 62157, A
30	51	44.0	831	15	US-10-360-101-236	Sequence 236, App
31	51	44.0	847	13	US-10-112-527-4	Sequence 4, Appl
32	51	44.0	1643	9	US-09-738-626-6894	Sequence 6894, Ap
33	51	44.0	1646	17	US-10-494-674-46	Sequence 46, Appl
34	50	43.1	844	15	US-10-424-599-260795	Sequence 260795, A
35	49	42.2	2017	15	US-10-114-270-86	Sequence 86, Appl
36	47	40.5	8	16	US-10-181-187D-6	Sequence 6, Appli
37	47	40.5	16	14	US-10-298-461-10	Sequence 10, Appl
38	47	40.5	19	16	US-10-181-187D-3	Sequence 3, Appli
39	47	40.5	215	14	US-10-298-461-30	Sequence 30, Appl
40	47	40.5	219	10	US-09-832-355A-24	Sequence 24, Appl
41	47	40.5	221	10	US-09-832-355A-21	Sequence 21, Appl
42	47	40.5	279	14	US-10-351-161A-46	Sequence 46, Appl
43	47	40.5	342	14	US-10-351-161A-48	Sequence 48, Appl
44	47	40.5	470	14	US-10-223-085-4	Sequence 4, Appli
45	47	40.5	470	14	US-10-223-084-4	Sequence 4, Appli
46	47	40.5	470	14	US-10-223-088-4	Sequence 4, Appli
47	47	40.5	470	14	US-10-223-090-4	Sequence 4, Appli
48	47	40.5	470	14	US-10-223-087-4	Sequence 4, Appli
49	47	40.5	470	14	US-10-223-083-4	Sequence 4, Appli
50	47	40.5	470	14	US-10-223-089-4	Sequence 4, Appli
51	47	40.5	470	14	US-10-394-557-6	Sequence 6, Appli
52	47	40.5	470	14	US-10-223-081-4	Sequence 4, Appli
53	47	40.5	470	14	US-10-223-082-4	Sequence 4, Appli
54	47	40.5	470	14	US-10-305-654-4	Sequence 4, Appli
55	47	40.5	470	15	US-10-081-056-4	Sequence 4, Appli
56	47	40.5	480	14	US-10-225-060-8	Sequence 8, Appli
57	47	40.5	496	9	US-09-998-831-4	Sequence 4, Appli
58	47	40.5	496	9	US-09-897-306-14	Sequence 14, Appl
59	47	40.5	496	10	US-09-998-833-4	Sequence 4, Appli
60	47	40.5	496	13	US-10-179-744-6	Sequence 6, Appli
61	47	40.5	496	14	US-10-186-817-6	Sequence 7, Appli
62	47	40.5	496	14	US-10-215-224-7	Sequence 7, Appli
63	47	40.5	496	14	US-10-215-224-8	Sequence 8, Appli
64	47	40.5	496	14	US-10-214-812-7	Sequence 7, Appli
65	47	40.5	496	14	US-10-214-812-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-989-920-185
; Sequence 185, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Pro
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22

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; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 185
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-920-185

Query Match      100.0%; Score 116; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGSWYSMRKXSMKIRPFPPQ 21
Db      469 KGSWYSMRKXSMKIRPFPPQ 489

RESULT 2
US-10-017-724-6
; Sequence 6, Application US/10017724
; Publication No. US2003009958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: WMI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-017-724-6

Query Match      100.0%; Score 116; DB 14; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGSWYSMRKXSMKIRPFPPQ 21
Db      471 KGSWYSMRKXSMKIRPFPPQ 491

RESULT 3
US-09-919-039-33
; Sequence 33, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 3393861CD1
US-09-919-039-33

Query Match      97.4%; Score 113; DB 10; Length 488;
Best Local Similarity 95.2%; Pred. No. 3.3e-08;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGSWYSMRKXSMKIRPFPPQ 21
Db      468 KGSWYSMRKXSMKIRPFPPQ 488

RESULT 4
US-10-181-187D-11
; Sequence 11, Application US/10181187D
; Publication No. US20040126758A1
; GENERAL INFORMATION:
; APPLICANT: GERARD MARX
; APPLICANT: RAPHAEL GORODETSKY
; TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES
; FILE REFERENCE: 10/181,187
; CURRENT APPLICATION NUMBER: US/10/181,187D
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US09/487790
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Haptotactic consensus sequence
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(16)
; OTHER INFORMATION: xaa is any amino acid or is absent
US-10-181-187D-11

Query Match      51.7%; Score 60; DB 16; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.083;
Matches 12; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

QY      1 KGSWYSMRKXSMKIRP 16
Db      1 KGXXYSMRKXXMKIRP 16

RESULT 5
US-10-181-187D-1
; Sequence 1, Application US/10181187D
; Publication No. US20040126758A1
; GENERAL INFORMATION:
; APPLICANT: GERARD MARX
; APPLICANT: RAPHAEL GORODETSKY
; TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES
; FILE REFERENCE: 10/181,187
; CURRENT APPLICATION NUMBER: US/10/181,187D
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US09/487790
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Equivalent to the c-terminus of fibrogen gamma-chain
US-10-181-187D-1

Query Match      51.7%; Score 60; DB 16; Length 20;
Best Local Similarity 64.7%; Pred. No. 0.1;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 KGSWYSMRKXSMKIRPF 17
Db      1 KTRWYSMKKTTWKIIPF 17
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RESULT 6
US-10-298-461-27
; Sequence 27, Application US/10298461
; Publication No. US20030215451A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Kowalski, Joe
; APPLICANT: Pisabarro, Maria Teresa
; APPLICANT: Sherman, Daniel Eric
; TITLE OF INVENTION: COMPOSITION COMPRISING AND METHOD OF
; TITLE OF INVENTION: USING ANGIOGENIC FACTOR ANGIOPOIETIN-LIKE PROTEIN 3 ANGPTL3
; FILE REFERENCE: GENENT.086A
; CURRENT APPLICATION NUMBER: US/10/298,461
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/333,429
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-461-27

Query Match 51.7%; Score 60; DB 14; Length 242;
Best Local Similarity 64.7%; Pred. No. 0.97;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPF 17
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Db 223 KTRWYSMKTKTKLIIP 239

RESULT 7
US-10-648-593-171
; Sequence 171, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-171

Query Match 51.7%; Score 60; DB 16; Length 437;
Best Local Similarity 64.7%; Pred. No. 1.7;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPF 17
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Db 399 KTRWYSMKTKTKLIIP 415

RESULT 8
US-10-733-969A-66
; Sequence 66, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE

; APPLICANT: HU, LIPING
; APPLICANT: LIU, TONG HUA
; APPLICANT: LU, ZHAO HUI
; APPLICANT: SHEN, YAN
; TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCRATIC CANCER
; FILE REFERENCE: 21525
; CURRENT APPLICATION NUMBER: US/10/733,969A
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 02028058.2
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Fibrinogen gamma chain precursor;
; OTHER INFORMATION: Accession NO: as of 29 August 2003: P02679
US-10-733-969A-66

Query Match 51.7%; Score 60; DB 17; Length 453;
Best Local Similarity 64.7%; Pred. No. 1.7;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPF 17
| | | | | : | | | | |
Db 399 KTRWYSMKTKTKLIIP 415

RESULT 9
US-10-372-735-41
; Sequence 41, Application US/10372735
; Publication No. US20030225251A1
; GENERAL INFORMATION:
; APPLICANT: Salberg, Matti
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUC4CPI*
; CURRENT APPLICATION NUMBER: US/10/372,735
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/234,579
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE95/00468
; PRIOR FILING DATE: 1995-04-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/664,025
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: PCT/IB01/02327
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 10/153,271
; PRIOR FILING DATE: 2002-05-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptides
US-10-372-735-41

Query Match 50.0%; Score 58; DB 14; Length 20;

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; Best Local Similarity 71.4%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17
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Db 2 WYSMKKTTMKIIPF 15

RESULT 10
US-10-608-541-41
; Sequence 41, Application US/10608541
; Publication No. US20040019189A1
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPEP.007CP3C1
; CURRENT APPLICATION NUMBER: US/10/608,541
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE 95/00468
; PRIOR FILING DATE: 1995-04-27
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Specificity domain peptide
US-10-608-541-41

Query Match 50.0%; Score 58; DB 15; Length 20;
Best Local Similarity 71.4%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17
   ||||| : |||||
Db 2 WYSMKKTTMKIIPF 15

RESULT 11
US-10-372-735-114
; Sequence 114, Application US/10372735
; Publication No. US20030225251A1
; GENERAL INFORMATION:
; APPLICANT: Sallberg, Matti
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUC4CP1
; CURRENT APPLICATION NUMBER: US/10/372,735
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/234,579
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE95/00468
; PRIOR FILING DATE: 1995-04-27

; Query Match 50.0%; Score 58; DB 15; Length 20;
; Best Local Similarity 71.4%; Pred. No. 0.2;
; Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

; Qy 4 WYSMRKMSMKIRPF 17
;   ||||| : |||||
; Db 2 WYSMKKTTMKIIPF 15

; RESULT 12
; US-10-608-541-102
; Sequence 102, Application US/10608541
; Publication No. US20040019189A1
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPEP.007CP3C1
; CURRENT APPLICATION NUMBER: US/10/608,541
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE 95/00468
; PRIOR FILING DATE: 1995-04-27
; PRIOR APPLICATION NUMBER: SE 9401460
; PRIOR FILING DATE: 1994-04-28
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ligand/Receptor specificity exchanger peptide
US-10-608-541-102

Query Match 50.0%; Score 58; DB 15; Length 27;
Best Local Similarity 71.4%; Pred. No. 0.26;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17
   ||||| : |||||
Db 2 WYSMKKTTMKIIPF 15

RESULT 13
US-10-181-187D-7
; Sequence 7, Application US/10181187D
```


;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

;; FILE REFERENCE: Aecomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 4553
;; LENGTH: 50
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AB020866.1
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 18
;; OTHER INFORMATION: SWISSPROT HIT: P12799, EVALUATE 1.00e-09
;; OTHER INFORMATION: EST_HUMAN HIT: AA677287.1, EVALUATE 5.00e-27

US-09-864-761-46553
Query Match 48.3%; Score 56; DB 9; Length 50;
Best Local Similarity 55.0%; Pred. No. 0.9;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GSWYSMRKMSMKIRP--FFP 19
| | | | | : | | | | | | | | | |
Db 30 GWWYSLKSVVMKIRPNDP 49

RESULT 17
US-09-992-600A-28
;; Sequence 28, Application US/0992600A
;; Publication No. US20030027161A1
;; GENERAL INFORMATION:
;; APPLICANT: Benjamin, Stephane
;; APPLICANT: Tanaka, Hiroaki
;; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

;; FILE REFERENCE: 91.US4.DIV
;; CURRENT APPLICATION NUMBER: US/09/992,600A
;; CURRENT FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 09/924,340
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: PCT/IB01/01715
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: US 60/305,456
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/302,277
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: US 60/298,698
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: US 60/293,574
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 114
;; SOFTWARE: JPatent
;; SEQ ID NO 28
;; LENGTH: 282
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: 116
;; OTHER INFORMATION: Xaa = Asn,Thr
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: 233
;; OTHER INFORMATION: Xaa = Phe,Ser
US-09-992-600A-28

Query Match 48.3%; Score 56; DB 10; Length 282;
Best Local Similarity 55.0%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GSWYSMRKMSMKIRP--FFP 19
| | | | | : | | | | | | | | | |
Db 260 GWWYSLKSVVMKIRPNDP 279

RESULT 18
US-09-924-340-28
;; Sequence 28, Application US/09924340
;; Publication No. US20030027248A1
;; GENERAL INFORMATION:
;; APPLICANT: Bejanin, Stephane
;; APPLICANT: Tanaka, Hiroaki
;; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;; FILE REFERENCE: 91.US2.REG
;; CURRENT APPLICATION NUMBER: US/09/924,340
;; CURRENT FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: US 60/305,456
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/302,277
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: US 60/298,698
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: US 60/293,574
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: JPatent
;; SEQ ID NO 28
;; LENGTH: 282
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: 116
;; OTHER INFORMATION: Xaa = Asn,Thr
;; NAME/KEY: UNSURE
;; LOCATION: 233
;; OTHER INFORMATION: Xaa = Phe,Ser
US-09-924-340-28

Query Match 48.3%; Score 56; DB 10; Length 282;
Best Local Similarity 55.0%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GSWYSMRKMSKIRP--FFP 19
| | | | : | | | | |
Db 260 GWYSLKSVVMKIRPNDFIP 279

RESULT 19

US-09-992-095B-28
; Sequence 28, Application US/09992095B
; Publication No. US20030157485A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US.DIV
; CURRENT APPLICATION NUMBER: US/09/992,095B
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 28
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: 116
; OTHER INFORMATION: Xaa = Asn,Thr
; NAME/KEY: MISC_FEATURE
; LOCATION: 233
; OTHER INFORMATION: Xaa = Phe,Ser
; US-09-992-095B-28

Query Match 48.3%; Score 56; DB 10; Length 282;
Best Local Similarity 55.0%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GSWYSMRKMSKIRP--FFP 19
| | | | : | | | | |
Db 260 GWYSLKSVVMKIRPNDFIP 279

RESULT 20

US-09-999-570-28
; Sequence 28, Application US/09999570
; Publication No. US20030170628A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: G-091US08DIV
; CURRENT APPLICATION NUMBER: US/09/999,570
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 28
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 116
; OTHER INFORMATION: Xaa = Asn,Thr
; NAME/KEY: UNSURE
; LOCATION: 233
; OTHER INFORMATION: Xaa = Phe,Ser
; US-09-999-570-28

Query Match 48.3%; Score 56; DB 10; Length 282;
Best Local Similarity 55.0%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GSWYSMRKMSKIRP--FFP 19
| | | | : | | | | |
Db 260 GWYSLKSVVMKIRPNDFIP 279

RESULT 21

US-10-000-489-28
; Sequence 28, Application US/10000489
; Publication No. US2003092011A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 28
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 116
; OTHER INFORMATION: Xaa = Asn,Thr
; NAME/KEY: UNSURE
; LOCATION: 233
; OTHER INFORMATION: Xaa = Phe,Ser
; US-10-000-489-28

Query Match 48.3%; Score 56; DB 14; Length 282;
Best Local Similarity 55.0%; Pred. No. 4.3;

Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | : : | | | | | |
Db 260 GWYSLKSVVMKIRPNDPFI 279

RESULT 22
US-10-000-986-28
; Sequence 28, Application US/10000986
; Publication No. US20030096247A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US9.DIV
; CURRENT APPLICATION NUMBER: US/10/000,986
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 28
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 116
; OTHER INFORMATION: Xaa = Asn,Thr
; NAME/KEY: UNSURE
; LOCATION: 233
; OTHER INFORMATION: Xaa = Phe,Ser
US-10-000-986-28

Query Match 48.3%; Score 56; DB 14; Length 282;
Best Local Similarity 55.0%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | : : | | | | | |
Db 260 GWYSLKSVVMKIRPNDPFI 279

RESULT 23
US-10-154-678-28
; Sequence 28, Application US/10154678
; Publication No. US20030162186A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 192.US1.REG
; CURRENT APPLICATION NUMBER: US/10/154,678
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 28
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 116
; OTHER INFORMATION: Xaa = Asn,Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 233
; OTHER INFORMATION: Xaa = Phe,Ser
US-10-154-678-28

Query Match 48.3%; Score 56; DB 14; Length 282;
Best Local Similarity 55.0%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | : : | | | | | |
Db 260 GWYSLKSVVMKIRPNDPFI 279

RESULT 24
US-09-925-301-1082
; Sequence 1082, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1082
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1082

Query Match 48.3%; Score 56; DB 9; Length 339;
Best Local Similarity 55.0%; Pred. No. 5.1;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | : : | | | | | |
Db 317 GWYSLKSVVMKIRPNDPFI 336

RESULT 25
US-09-832-355A-23
; Sequence 23, Application US/09832355A
; Publication No. US20030027751A1
; GENERAL INFORMATION:
; APPLICANT: Kovessi, Imre
; APPLICANT: Kessler, Paul
; TITLE OF INVENTION: VEGF FUSION PROTEINS
; FILE REFERENCE: 205654
; CURRENT APPLICATION NUMBER: US/09/832,355A
; CURRENT FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-355A-23

Query Match 44.8%; Score 52; DB 10; Length 217;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSWYSMRKMSMKIRP 16
Db 198 GSTYSLKRVENKIRP 212
|||:::|||||

RESULT 26

US-10-112-527-3
; Sequence 3, Application US/10112527
; Publication No. US20020168722A1
; GENERAL INFORMATION:
; APPLICANT: Griening, Gerd
; APPLICANT: Applegate, Dianne
; APPLICANT: Stoike-Steben, Lara
; TITLE OF INVENTION: No. US20020168722A1 Cleaved Fragments of Fibrinogen
; FILE REFERENCE: Docket 454-24 CON
; CURRENT APPLICATION NUMBER: US/10/112,527
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/373,157
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-527-3

Query Match 44.0%; Score 51; DB 13; Length 221;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPFPQ 20
Db 202 RGADYSLRAVRMKIRPLVTQ 221
:::|:::|||||

RESULT 27

US-10-112-527-2
; Sequence 2, Application US/10112527
; Publication No. US20020168722A1
; GENERAL INFORMATION:
; APPLICANT: Griening, Gerd
; APPLICANT: Applegate, Dianne
; APPLICANT: Stoike-Steben, Lara
; TITLE OF INVENTION: No. US20020168722A1 Cleaved Fragments of Fibrinogen
; FILE REFERENCE: Docket 454-24 CON
; CURRENT APPLICATION NUMBER: US/10/112,527
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/373,157
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-527-2

Query Match 44.0%; Score 51; DB 13; Length 236;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPFPQ 20
Db 217 RGADYSLRAVRMKIRPLVTQ 236
:::|:::|||||

RESULT 28

US-10-112-527-1
; Sequence 1, Application US/10112527
; Publication No. US20020168722A1
; GENERAL INFORMATION:
; APPLICANT: Griening, Gerd
; APPLICANT: Applegate, Dianne
; APPLICANT: Stoike-Steben, Lara
; TITLE OF INVENTION: No. US20020168722A1 Cleaved Fragments of Fibrinogen
; FILE REFERENCE: Docket 454-24 CON
; CURRENT APPLICATION NUMBER: US/10/112,527
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/373,157
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-527-1

Query Match 44.0%; Score 51; DB 13; Length 251;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPFPQ 20
Db 232 RGADYSLRAVRMKIRPLVTQ 251
:::|:::|||||

RESULT 29

US-10-282-122A-62157
; Sequence 62157, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

US-10-282-122A-62157
; Sequence 62157, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EUTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931

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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62157
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-62157

Query Match          44.0%; Score 51; DB 15; Length 471;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SWYSMRKMSMKIRP 16
Db 317 SWYEQRETSLKMRP 330

RESULT 30
US-10-360-101-236
; Sequence 236, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 236
; LENGTH: 831
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of fibrinogen
US-10-360-101-236

Query Match          44.0%; Score 51; DB 15; Length 831;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 10; Conservative 4; Mismatches 6; Indels 6; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPFPQ 20
Db 812 RGADYSLRAVRMKIRPLVTQ 831

RESULT 31
US-10-112-527-4
; Sequence 4, Application US/10112527
; Publication No. US20020168722A1
; GENERAL INFORMATION:
; APPLICANT: Griening, Gerd
; APPLICANT: Applegate, Dianne
; TITLE OF INVENTION: No. US20020168722A1 Cleaved Fragments of Fibrinogen
; FILE REFERENCE: Docket 454-24 CON
; CURRENT APPLICATION NUMBER: US/10/112,527
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/373,157
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 847
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-527-4

Query Match          44.0%; Score 51; DB 13; Length 847;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPFPQ 20
Db 828 RGADYSLRAVRMKIRPLVTQ 847

RESULT 32
US-09-738-626-6894
; Sequence 6894, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6894
; LENGTH: 1643
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6894

Query Match          44.0%; Score 51; DB 9; Length 1643;
Best Local Similarity 37.8%; Pred. No. 1.1e+02;
Matches 14; Conservative 1; Mismatches 6; Indels 16; Gaps 1;

QY 1 KGSWYSMRKMSMK-----IRPFPQ 21
Db 1297 KISWDSNLKMSLSRGDTFSFDPSSIQMSLYRPFPPQ 1333

RESULT 33
US-10-494-674-46
; Sequence 46, Application US/10494674
; Publication No. US20040259215A1
; GENERAL INFORMATION:
; APPLICANT: Zelder, Oskar
; APPLICANT: Pompejue, Markus
; APPLICANT: Schroder, Hartwig
; APPLICANT: Kroger, Burkhard
; APPLICANT: Klopprogge, Corinna
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: Genes coding for DNA replication and pathogenesis proteins
; FILE REFERENCE: BGI-168US
; CURRENT APPLICATION NUMBER: US/10/494,674
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: PCT/EP02/12132
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: DE 10154246
```


;; PRIOR FILING DATE: 2001-11-05
;; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 46

LENGTH: 1646

TYPE: PRT

;; ORGANISM: Corynebacterium glutamicum
US-10-494-674-46

Query Match 44.0%; Score 51; DB 17; Length 1646;

Best Local Similarity 37.8%; Pred. No. 1.1e+02;

Matches 14; Conservative 1; Mismatches 6; Indels 16; Gaps 1;

Qy 1 KGSWSMRKMSMK-----IRPFPPQ 21

Db 1300 KISWNSLKMSLRGDTFDPSSIQMSLYRPFPPQ 1336

RESULT 34

US-10-424-599-260795

;; Sequence 260795, Application US/10424599

;; Publication No. US20040031072A1

;; GENERAL INFORMATION:

;; APPLICANT: La Rosa Thomas J

;; APPLICANT: Kovalic David K

;; APPLICANT: Zhou Yihua

;; APPLICANT: Cao Yongwei

;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

;; FILE REFERENCE: 38-21(53223)B

;; CURRENT APPLICATION NUMBER: US/10/424,599

;; CURRENT FILING DATE: 2003-04-28

;; NUMBER OF SEQ ID NOS: 285684

;; SEQ ID NO 260795

LENGTH: 844

TYPE: PRT

;; ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(844)

;; OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

;; OTHER INFORMATION: Clone ID: PAT_MRT3847_77520C.1.pep

US-10-424-599-260795

Query Match 43.1%; Score 50; DB 15; Length 844;

Best Local Similarity 56.2%; Pred. No. 87;

Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GSWYSMRKMSMKIRPF 17

Db 786 GSYLTLEKMMWIRPF 801

RESULT 35

US-10-114-270-86

;; Sequence 86, Application US/10114270

;; Publication No. US20040030110A1

;; GENERAL INFORMATION:

;; APPLICANT: Guo, Xiaojia

;; APPLICANT: Kekuda, Ramesh

;; APPLICANT: Miller, Charles E.

;; APPLICANT: Malyankar, Uriel M.

;; APPLICANT: Spytek, Kimberly A.

;; APPLICANT: Patturajan, Meera

;; APPLICANT: Liu, Zhaozhong

;; APPLICANT: Gusev, Vladimir Y.

;; APPLICANT: Li, Li

;; APPLICANT: Vernet, Corine

;; APPLICANT: Zerhusen, Bryan D.

;; APPLICANT: Gorman, Linda

;; APPLICANT: Shenoy, Suresh G.

;; APPLICANT: Pena, Carol E.A.

;; APPLICANT: Smithson, Glenda

;; APPLICANT: Burgess, Catherine E.
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Shimkets, Richard A.
;; APPLICANT: Gangolli, Baha A.
;; APPLICANT: Taupier Jr., Raymond J.
;; APPLICANT: Casman, Stacie J.
;; APPLICANT: Ji, Weizhen
;; APPLICANT: Anderson, David W.
;; APPLICANT: Liete, Mario W.
;; APPLICANT: Rastelli, Luca
;; APPLICANT: Edinger, Shlomit R.
;; APPLICANT: Stone, David J.
;; APPLICANT: MacDougall, John R.
;; APPLICANT: Rothenberg, Mark E.
;; TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same

;; FILE REFERENCE: 21402-322C

;; CURRENT APPLICATION NUMBER: US/10/114,270

;; CURRENT FILING DATE: 2002-11-27

;; PRIOR APPLICATION NUMBER: 60/281,086

;; PRIOR FILING DATE: 2001-04-03

;; PRIOR APPLICATION NUMBER: 60/281,136

;; PRIOR FILING DATE: 2001-04-03

;; PRIOR APPLICATION NUMBER: 60/281,863

;; PRIOR FILING DATE: 2001-04-05

;; PRIOR APPLICATION NUMBER: 60/281,906

;; PRIOR FILING DATE: 2001-04-05

;; PRIOR APPLICATION NUMBER: 60/282,020

;; PRIOR FILING DATE: 2001-04-06

;; PRIOR APPLICATION NUMBER: 60/282,930

;; PRIOR FILING DATE: 2001-04-10

;; PRIOR APPLICATION NUMBER: 60/282,934

;; PRIOR FILING DATE: 2001-04-10

;; PRIOR APPLICATION NUMBER: 60/283,512

;; PRIOR FILING DATE: 2001-04-12

;; PRIOR APPLICATION NUMBER: 60/283,710

;; PRIOR FILING DATE: 2001-04-13

;; PRIOR APPLICATION NUMBER: 60/284,234

;; PRIOR FILING DATE: 2001-04-17

;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 470

;; SEQ ID NO 86

LENGTH: 2017

TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-114-270-86

Query Match 42.2%; Score 49; DB 15; Length 2017;

Best Local Similarity 47.4%; Pred. No. 2.7e+02;

Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GSWYSMRKMSMKIRPFPPQ 20

Db 1709 GRWASYRNMGDLFGFPYPQ 1727

RESULT 36

US-10-181-187D-6

;; Sequence 6, Application US/10181187D

;; Publication No. US20040126758A1

;; GENERAL INFORMATION:

;; APPLICANT: GERARD MARX

;; APPLICANT: RAPHAEL GORODETSKY

;; TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES

;; FILE REFERENCE: 10/181,187

;; CURRENT APPLICATION NUMBER: US/10/181,187D

;; CURRENT FILING DATE: 2003-10-20

;; PRIOR APPLICATION NUMBER: US09/487790

;; PRIOR FILING DATE: 2000-01-20

;; NUMBER OF SEQ ID NOS: 12

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 6

LENGTH: 8

```
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Equivalent to the c-terminus of fibrinogen beta-chain
US-10-181-187D-6

Query Match          40.5%; Score 47; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGSWYSMR 8
   |||||
Db 1 KGSWYSMR 8

RESULT 37
US-10-298-461-10
; Sequence 10, Application US/10298461
; Publication No. US20030215451A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Kowalski, Joe
; APPLICANT: Pisabarro, Maria Teresa
; APPLICANT: Sherman, Daniel Eric
; TITLE OF INVENTION: COMPOSITION COMPRISING AND METHOD OF
; FILE REFERENCE: GENENT.086A
; CURRENT APPLICATION NUMBER: US/10/298,461
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/332,429
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-461-10

Query Match          40.5%; Score 47; DB 14; Length 16;
Best Local Similarity 69.2%; Pred. No. 6.6;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 YSMRKMMSMKIRPF 17
   |||:| :|||
Db 1 YSMKKTMTMKIIPF 13

RESULT 38
US-10-181-187D-3
; Sequence 3, Application US/10181187D
; Publication No. US20040126759A1
; GENERAL INFORMATION:
; APPLICANT: GERARD MARX
; APPLICANT: RAPHAEL GORODETSKY
; TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES
; FILE REFERENCE: 10/181,187
; CURRENT APPLICATION NUMBER: US/10/181,187D
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US09/487790
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Equivalent to the c-terminus of angiopoietin-2
US-10-181-187D-3

Query Match          40.5%; Score 47; DB 16; Length 19;
```

```
Best Local Similarity 56.2%; Pred. No. 7.7;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMMSMKIRP 16
   |||||:| :|||
Db 1 KGSGYSLKATMTMIRP 16

RESULT 39
US-10-298-461-30
; Sequence 30, Application US/10298461
; Publication No. US20030215451A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Kowalski, Joe
; APPLICANT: Pisabarro, Maria Teresa
; APPLICANT: Sherman, Daniel Eric
; TITLE OF INVENTION: COMPOSITION COMPRISING AND METHOD OF
; FILE REFERENCE: GENENT.086A
; CURRENT APPLICATION NUMBER: US/10/298,461
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/332,429
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-461-30

Query Match          40.5%; Score 47; DB 14; Length 215;
Best Local Similarity 56.2%; Pred. No. 69;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMMSMKIRP 16
   |||||:| :|||
Db 197 KGSGYSLKATMTMIRP 212

RESULT 40
US-09-832-355A-24
; Sequence 24, Application US/09832355A
; Publication No. US20030027751A1
; GENERAL INFORMATION:
; APPLICANT: Kovesdi, Imre
; APPLICANT: Kessler, Paul
; TITLE OF INVENTION: VEGF FUSION PROTEINS
; FILE REFERENCE: 205654
; CURRENT APPLICATION NUMBER: US/09/832,355A
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-355A-24

Query Match          40.5%; Score 47; DB 10; Length 219;
Best Local Similarity 56.2%; Pred. No. 70;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMMSMKIRP 16
   :|||:| :|||
Db 201 RGGAYSLRKAAMLRP 216

RESULT 41
US-09-832-355A-21
; Sequence 21, Application US/09832355A
```

```
; Publication No. US20030027751A1
; GENERAL INFORMATION:
; APPLICANT: Kovesdi, Imre
; APPLICANT: Kessler, Paul
; TITLE OF INVENTION: VEGF FUSION PROTEINS
; FILE REFERENCE: 205654
; CURRENT APPLICATION NUMBER: US/09/832,355A
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-355A-21

Query Match      40.5%; Score 47; DB 10; Length 221;
Best Local Similarity 56.2%; Pred. No. 71;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRP 16
Db      203 KGSYSLKATTTMIRP 218

RESULT 42
US-10-351-161A-46
; Sequence 46, Application US/10351161A
; Publication No. US20030228659A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Montgomery, Julie
; TITLE OF INVENTION: No. US20030228659A1el Angiopoietin Materials and Methods
; FILE REFERENCE: 28110/35663CON
; CURRENT APPLICATION NUMBER: US/10/351.161A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/354,881
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-351-161A-46

Query Match      40.5%; Score 47; DB 14; Length 279;
Best Local Similarity 56.2%; Pred. No. 88;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRP 16
Db      261 RGGAYSLRKAAMLIRP 276

RESULT 43
US-10-351-161A-48
; Sequence 48, Application US/10351161A
; Publication No. US20030228659A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Montgomery, Julie
; TITLE OF INVENTION: No. US20030228659A1el Angiopoietin Materials and Methods
; FILE REFERENCE: 28110/35663CON
; CURRENT APPLICATION NUMBER: US/10/351.161A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/354,881
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-351-161A-48

Query Match      40.5%; Score 47; DB 14; Length 342;
Best Local Similarity 56.2%; Pred. No. 1.1e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRP 16
Db      324 RGGAYSLRKAAMLIRP 339

RESULT 44
US-10-223-085-4
; Sequence 4, Application US/10223085
; Publication No. US20030100497A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C10
; CURRENT APPLICATION NUMBER: US/10/223.085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-085-4

Query Match      40.5%; Score 47; DB 14; Length 470;
Best Local Similarity 56.2%; Pred. No. 1.4e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRP 16
Db      452 RGGAYSLRKAAMLIRP 467
```



```
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C2
; CURRENT APPLICATION NUMBER: US/10/223,090
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-090-4

Query Match 40.58; Score 47; DB 14; Length 470;
Best Local Similarity 56.28; Pred. No. 1.4e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWSYMRKMSMKIRP 16
   :|||:|:|:|
Db 452 RGGAYSLRKAAMLRP 467

RESULT 48
US-10-223-087-4
; Sequence 4, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C4
; CURRENT APPLICATION NUMBER: US/10/223,087
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
```

```
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/232,887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2005, 11:04:01 ; Search time 38 seconds
(without alignments)
36.649 Million cell updates/sec

Title: US-09-487-790A-1

Perfect score: 116

Sequence: 1 KGSWSMRKXMKIRPFPPQ 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*

6: /cgn2_6/ptodata/1/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	100.0	491	US-08-206-176-4	Sequence 4, Appli
2	113	97.4	488	US-09-919-039-33	Sequence 33, Appl
3	60	51.7	453	US-08-206-176-6	Sequence 6, Appli
4	60	51.7	454	US-08-434-099A-27	Sequence 27, Appl
5	60	51.7	454	US-08-434-099A-28	Sequence 28, Appl
6	58	50.0	20	US-09-664-945-41	Sequence 41, Appl
7	58	50.0	21	US-08-397-633A-37	Sequence 37, Appl
8	58	50.0	27	US-09-664-945-102	Sequence 102, App
9	58	50.0	73	US-08-642-255-127	Sequence 127, App
10	58	50.0	73	US-08-397-633A-38	Sequence 38, Appl
11	58	50.0	75	US-08-642-255-130	Sequence 130, App
12	58	50.0	75	US-08-397-633A-47	Sequence 47, Appl
13	58	50.0	198	US-08-642-255-131	Sequence 131, App
14	58	50.0	198	US-08-397-633A-41	Sequence 41, Appl
15	58	50.0	198	US-08-397-633A-52	Sequence 52, Appl
16	58	50.0	314	US-08-525-505A-2	Sequence 2, Appli
17	57	49.1	411	US-08-232-532-1	Sequence 1, Appli
18	57	49.1	411	US-08-748-150-1	Sequence 1, Appli
19	57	49.1	411	US-09-347-877-1	Sequence 1, Appli
20	57	49.1	411	US-09-912-740A-1	Sequence 1, Appli
21	57	49.1	411	US-09-912-741B-1	Sequence 1, Appli
22	57	49.1	411	PCT-US95-05168-1	Sequence 1, Appli
23	56	48.3	282	US-10-000-489-28	Sequence 28, Appl
24	56	48.3	312	US-08-525-505A-4	Sequence 4, Appli
25	56	48.3	312	US-09-976-594-1009	Sequence 1009, Ap
26	52	44.8	346	US-08-960-507-19	Sequence 19, Appl
27	52	44.8	346	US-09-136-801-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-206-176-4
; Sequence 4, Application US/08206176
; Patent No. 5639940
; GENERAL INFORMATION:
; APPLICANT: Garnet, Ian
; APPLICANT: Dalrymple, Michael A
; APPLICANT: Prunkard, Donna E
; APPLICANT: Foster, Donald C
; TITLE OF INVENTION: Production of Fibrinogen in Transgenic
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,176
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E

Sequence 19, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 4890, Ap
Sequence 6, Appli
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Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 8, Appli
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Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli

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; ; REGISTRATION NUMBER: 31-648
; ; REFERENCE/DOCKET NUMBER: 93-15
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 206-547-8080 ext 322
; ; TELEFAX: 206-548-2329
; ; INFORMATION FOR SEQ ID NO: 4:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 491 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; US-08-206-176-4

Query Match 100.0%; Score 116; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPFPPQQ 21
Db 471 KGSWYSMRKMSMKIRPFPPQQ 491

RESULT 2
US-09-919-039-33
; Sequence 33, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; ; APPLICANT: Kaser, Matthew R.
; ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; ; FILE REFERENCE: PA-0035 US
; ; CURRENT APPLICATION NUMBER: US/09/919,039
; ; CURRENT FILING DATE: 2002-09-09
; ; PRIOR APPLICATION NUMBER: 60/222,113
; ; PRIOR FILING DATE: 2000-07-28
; ; NUMBER OF SEQ ID NOS: 401
; ; SOFTWARE: PERL Program
; ; SEQ ID NO 33
; ; LENGTH: 488
; ; TYPE: PRT
; ; ORGANISM: Homo sapiens
; ; FEATURE:
; ; NAME/KEY: misc feature
; ; OTHER INFORMATION: Incyte ID No. 6727066 3393861CD1
US-09-919-039-33

Query Match 97.4%; Score 113; DB 4; Length 488;
Best Local Similarity 95.2%; Pred. No. 1e-10;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPFPPQQ 21
Db 468 KGSWYSMRKMSMKIRPFPPQQ 488

RESULT 3
US-08-206-176-6
; Sequence 6, Application US/08206176
; Patent No. 5639940
; GENERAL INFORMATION:
; ; APPLICANT: Garner, Ian
; ; APPLICANT: Dallymple, Michael A
; ; APPLICANT: Prunkard, Donna E
; ; APPLICANT: Foster, Donald C
; ; TITLE OF INVENTION: Production of Fibrinogen in Transgenic
; ; TITLE OF INVENTION: Animals
; ; NUMBER OF SEQUENCES: 27
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: ZymoGenetics, Inc.
; ; STREET: 4225 Roosevelt Way, N.E.
; ; CITY: Seattle
; ; STATE: WA
; ; COUNTRY: USA
; ; ZIP: 98105
```

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; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; COMPUTER: IBM PC compatible
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: Patent In Release #1.0, Version #1.25
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/08/206,176
; ; FILING DATE:
; ; CLASSIFICATION: 435
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Parker, Gary E
; ; REGISTRATION NUMBER: 31-648
; ; REFERENCE/DOCKET NUMBER: 93-15
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 206-547-8080 ext 322
; ; TELEFAX: 206-548-2329
; ; INFORMATION FOR SEQ ID NO: 6:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 453 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; US-08-206-176-6

Query Match 51.7%; Score 60; DB 1; Length 453;
Best Local Similarity 64.7%; Pred. No. 0.066;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSMKIRPF 17
Db 399 KTRWYSMKKTTMKLIFF 415

RESULT 4
US-08-434-099A-27
; Sequence 27, Application US/08434099A
; Patent No. 6081902
; GENERAL INFORMATION:
; ; APPLICANT: Cederholm-Wms., Stewart A.
; ; TITLE OF INVENTION: Recombinant Fibrin Chains,
; ; TITLE OF INVENTION: Fibrin and Fibrin-Homologs
; ; NUMBER OF SEQUENCES: 37
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: E.R. Squibb & Sons, Inc.
; ; STREET: 100 Headquarters Park Drive
; ; CITY: Skillman
; ; STATE: NJ
; ; COUNTRY: USA
; ; ZIP: 08558
; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Diskette
; ; COMPUTER: IBM Compatible
; ; OPERATING SYSTEM: DOS
; ; SOFTWARE: FastSeq for Windows Version 2.0
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/08/434,099A
; ; FILING DATE: 03-MAY-1995
; ; CLASSIFICATION: 435
; ; PRIOR APPLICATION NUMBER:
; ; APPLICATION NUMBER: US 08/236,979
; ; FILING DATE: 02-MAY-1994
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Furman, Jr., Esq., Theodore R
; ; REGISTRATION NUMBER: 30,942
; ; REFERENCE/DOCKET NUMBER: CV0054a
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 908-281-2372
; ; TELEFAX: 908-281-2373
; ; TELEX:
; ; INFORMATION FOR SEQ ID NO: 27:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 454 amino acids
; ; TYPE: amino acid
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```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-434-099A-27

Query Match          51.7%; Score 60; DB 3; Length 454;
Best Local Similarity 64.7%; Pred. No. 0.066;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 KGSWYSMRKSMKIRPF 17
Db 416 KTRYSMKTKTKIIPF 432

RESULT 5
US-08-434-099A-28
; Sequence 28, Application US/08434099A
; Patent No. 6083902
; GENERAL INFORMATION:
; APPLICANT: Cederholm-Wms., Stewart A.
; TITLE OF INVENTION: Recombinant Fibrin Chains,
; TITLE OF INVENTION: Fibrin and Fibrin-Homologs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.R. Squibb & Sons, Inc.
; STREET: 100 Headquarters Park Drive
; CITY: Skillman
; STATE: NJ
; COUNTRY: USA
; ZIP: 08558
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,099A
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,979
; FILING DATE: 02-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Jr., Esq., Theodore R
; REGISTRATION NUMBER: 30,942
; REFERENCE/DOCKET NUMBER: CV0054a
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-281-2372
; TELEFAX: 908-281-2373
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-434-099A-28

Query Match          51.7%; Score 60; DB 3; Length 454;
Best Local Similarity 64.7%; Pred. No. 0.066;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 KGSWYSMRKSMKIRPF 17
Db 416 KTRYSMKTKTKIIPF 432

RESULT 6
US-09-664-945-41
; Sequence 41, Application US/09664945
; Patent No. 6660842
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPEP.007CP3
; CURRENT APPLICATION NUMBER: US/09/664,945
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: SE 9401460
; PRIOR FILING DATE: 1994-04-28
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Specificity domain peptide
US-09-664-945-41

Query Match          50.0%; Score 58; DB 4; Length 20;
Best Local Similarity 71.4%; Pred. No. 0.005;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 4 WYSMRKSMKIRPF 17
Db 2 WYSMKTKTKIIPF 15

RESULT 7
US-08-397-633A-37
; Sequence 37, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-397-633A-37

Query Match 50.0%; Score 58; DB 1; Length 21;
Best Local Similarity 71.4%; Pred. No. 0.0053;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
Db 3 WYSMKTTMKIIPF 16

RESULT 8

US-09-664-945-102
; Sequence 102, Application US/09664945
; Patent No. 6660842
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPEP.007CP3
; CURRENT APPLICATION NUMBER: US/09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: SE 9401460
; PRIOR FILING DATE: 1994-04-28
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ligand/Receptor specificity exchanger peptide
US-09-664-945-102

Query Match 50.0%; Score 58; DB 4; Length 27;
Best Local Similarity 71.4%; Pred. No. 0.0069;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
Db 2 WYSMKTTMKIIPF 15

RESULT 9

US-08-642-255-127
; Sequence 127, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; TITLE OF INVENTION: Protein Polymers
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255

; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-642-255-127

Query Match 50.0%; Score 58; DB 1; Length 73;
Best Local Similarity 71.4%; Pred. No. 0.02;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 WYSMRKMSMKIRPF 17
Db 35 WYSMKTTMKIIPF 48

RESULT 10

US-08-397-633A-38
; Sequence 38, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-38

Query Match 50.0%; Score 58; DB 1; Length 73;
Best Local Similarity 71.4%; Pred. No. 0.02;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17
 |||||:|||||
 Db 35 WYSMKTKTKIIPF 48

RESULT 11

US-08-642-255-130
 ; Sequence 130, Application US/08642255
 ; Patent No. 5773249
 ; GENERAL INFORMATION:
 ; APPLICANT: CAPPELLO, Joseph
 ; TITLE OF INVENTION: High Molecular Weight Collagen-Like
 ; TITLE OF INVENTION: High Molecular Weight Collagen-Like
 ; NUMBER OF SEQUENCES: 135
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ROWLAND, Bertram I.
 ; REGISTRATION NUMBER: 20,015
 ; REFERENCE/DOCKET NUMBER: A55556-3/BIR
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 494-8700
 ; TELEFAX: (415) 494-8771
 ; TELEX: 910 277299 FHT UR
 ; INFORMATION FOR SEQ ID NO: 130:
 ; LENGTH: 75 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-642-255-130

Query Match 50.0%; Score 58; DB 1; Length 75;
 Best Local Similarity 71.4%; Pred. No. 0.021;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17
 |||||:|||||
 Db 35 WYSMKTKTKIIPF 48

RESULT 12

US-08-397-633A-47
 ; Sequence 47, Application US/08397633A
 ; Patent No. 5773577
 ; GENERAL INFORMATION:
 ; APPLICANT: CAPPELLO, Joseph
 ; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
 ; TITLE OF INVENTION: OF ENZYMIC CROSS-LINKING
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA

ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ROWLAND, Bertram I.
 ; REGISTRATION NUMBER: 20,015
 ; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 47:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 75 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-397-633A-47

Query Match 50.0%; Score 58; DB 1; Length 75;
 Best Local Similarity 71.4%; Pred. No. 0.021;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WYSMRKMSMKIRPF 17
 |||||:|||||
 Db 35 WYSMKTKTKIIPF 48

RESULT 13

US-08-642-255-131
 ; Sequence 131, Application US/08642255
 ; Patent No. 5773249
 ; GENERAL INFORMATION:
 ; APPLICANT: CAPPELLO, Joseph
 ; TITLE OF INVENTION: High Molecular Weight Collagen-Like
 ; TITLE OF INVENTION: Protein Polymers
 ; NUMBER OF SEQUENCES: 135
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ROWLAND, Bertram I.
 ; REGISTRATION NUMBER: 20,015
 ; REFERENCE/DOCKET NUMBER: A55556-3/BIR
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 494-8700
 ; TELEFAX: (415) 494-8771
 ; TELEX: 910 277299 FHT UR
 ; INFORMATION FOR SEQ ID NO: 131:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 198 amino acids

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-642-255-131

Query Match          50.0%; Score 58; DB 1; Length 198;
Best Local Similarity 71.4%; Pred. No. 0.059; 2; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 2;

QY 4 WYSMRKXSMKIRPF 17
Db 68 WYSMKTKTKIIPF 81

RESULT 14
US-08-397-633A-41
; Sequence 41, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-633A-52

Query Match          50.0%; Score 58; DB 1; Length 198;
Best Local Similarity 71.4%; Pred. No. 0.059; 2; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 2;

QY 4 WYSMRKXSMKIRPF 17
Db 68 WYSMKTKTKIIPF 81

RESULT 15
US-08-397-633A-52
; Sequence 52, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-633A-41

Query Match          50.0%; Score 58; DB 1; Length 198;
Best Local Similarity 71.4%; Pred. No. 0.059; 2; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 2;

QY 4 WYSMRKXSMKIRPF 17
Db 68 WYSMKTKTKIIPF 81

RESULT 16
US-08-525-505A-2
; Sequence 2, Application US/08525505A
; Patent No. 5807711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: MATSUKI, YUMIKO
; APPLICANT: SHINDO, SAKAO
; APPLICANT: HANADA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
```



```
; Sequence 1, Application US/09912741B
; Patent No. 6737058
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C
; APPLICANT: Languino, Lucia R
; APPLICANT: Thornton, George B
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
; TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION
; FILE REFERENCE: 300.1D1v4
; CURRENT APPLICATION NUMBER: US/09/912,741B
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 09/347,877
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 08/748,150
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: US 08/232,532
; PRIOR FILING DATE: 1994-04-25
; PRIOR APPLICATION NUMBER: US 08/139,562
; PRIOR FILING DATE: 1993-10-19
; PRIOR APPLICATION NUMBER: US 07/898,117
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: expressed
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: 88
; OTHER INFORMATION: site of glycosylation
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (153)...(182)
; OTHER INFORMATION: disulfide-bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (326)...(339)
; OTHER INFORMATION: disulfide-bond
; US-09-912-741B-1

Query Match 49.1%; Score 57; DB 4; Length 411;
Best Local Similarity 64.7%; Pred. No. 0.19;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPF 17
| | | | | | | | | |
Db 373 KTRWYSMKTKIMKIIPF 389

RESULT 22
PCT-US95-05168-1
; Sequence 1, Application PC/TUS9505168
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
; TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05168
; FILING DATE: 24-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/232,532
; FILING DATE: 25-APR-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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```
; LENGTH: 411 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 88
; OTHER INFORMATION: /note= "SITE OF GLYCOSYLATION"
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 153..182
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 326..339
; PCT-US95-05168-1

Query Match 49.1%; Score 57; DB 5; Length 411;
Best Local Similarity 64.7%; Pred. No. 0.19;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPF 17
| | | | | | | | | |
Db 373 KTRWYSMKTKIMKIIPF 389

RESULT 23
US-10-000-489-28
; Sequence 28, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 28
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 116
; OTHER INFORMATION: Xaa = Asn,Thr
; NAME/KEY: UNSURE
; LOCATION: 233
; OTHER INFORMATION: Xaa = Phe,Ser
; US-10-000-489-28

Query Match 48.3%; Score 56; DB 4; Length 282;
Best Local Similarity 55.0%; Pred. No. 0.19;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GSWYSMRKMSMKIRP--FFP 19
| | | | | | | | | |
Db 260 GWYSLKSVVMKIRPNDP 279

RESULT 24
```

US-08-525-505A-4
; Sequence 4, Application US/08525505A
; Patent No. 5807711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: MATSUKI, YUMIKO
; APPLICANT: SHINDO, SAEKO
; APPLICANT: HANADA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPATOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C. JEFFERSON DAVIS HIGHWAY, SUITE 400
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00455
; FILING DATE: 22-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-063905
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-505A-4

Query Match 48.3%; Score 56; DB 1; Length 312;
Best Local Similarity 55.0%; Pred. No. 0.21;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | | : | | | | |
Db 290 GWWYSLKSVVMKIRPNDP 309

RESULT 25
US-09-976-594-1009
; Sequence 1009, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program

; SEQ ID NO 1009
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 029251CDI
US-09-976-594-1009

Query Match 48.3%; Score 56; DB 4; Length 312;
Best Local Similarity 55.0%; Pred. No. 0.21;
Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 GSWYSMRKMSMKIRP--FFP 19
| | | | | : | | | | |
Db 290 GWWYSLKSVVMKIRPNDP 309

RESULT 26
US-08-960-507-19
; Sequence 19, Application US/08960507
; Patent No. 6057435
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,507
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130p1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-960-507-19

Query Match 44.8%; Score 52; DB 3; Length 346;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSWYSMRKMSMKIRP 16
| | | | | : | | | | |
Db 327 GSTYSLKRVEMKIRP 341

RESULT 27
US-09-136-801-19
; Sequence 19, Application US/09136801
; Patent No. 6413770
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA: US/09/136.801
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-801-19

Query Match 44.8%; Score 52; DB 4; Length 346;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSWYSMRKMSMKIRP 16
|||:::|||||
Db 327 GSTYSLKRVEMKIRP 341

RESULT 28
US-09-202-088A-19
Sequence 19, Application US/09202088A
Patent No. 6551822
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: TIE LIGAND HOMOLOGUES
FILE REFERENCE: P1130P3US
CURRENT APPLICATION NUMBER: US/09/202,088A
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 19
LENGTH: 346
TYPE: PRT
ORGANISM: Homo Sapiens

US-09-202-088A-19
Query Match 44.8%; Score 52; DB 4; Length 346;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GSWYSMRKMSMKIRP 16
|||:::|||||
Db 327 GSTYSLKRVEMKIRP 341
RESULT 29
US-08-886-269-7
Sequence 7, Application US/08886269
Patent No. 6025148
GENERAL INFORMATION:
APPLICANT: Grieninger, Gerd
APPLICANT: Fu, Yiping
APPLICANT: Cao, Yan
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Kudryk, Bohdan J.
TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
FILE REFERENCE: Sequences 1-7 for 454-7 CON/CPA
CURRENT APPLICATION NUMBER: US/08/886,269
CURRENT FILING DATE: 1997-07-01
EARLIER APPLICATION NUMBER: 08/479,755
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
US-08-886-269-7
Query Match 44.0%; Score 51; DB 3; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRPPFPQ 20
::||:::|||||
Db 8 RGADYSLRAVRMKIRPLVTQ 27

RESULT 30
US-09-167-647-7
Sequence 7, Application US/09167647
Patent No. 6025476
GENERAL INFORMATION:
APPLICANT: Grieninger, Gerd
APPLICANT: Fu, Yiping
APPLICANT: Cao, Yan
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Kudryk, Bohdan J.
TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
FILE REFERENCE: Seq.ID #1 - 7 454-7 DIV
CURRENT APPLICATION NUMBER: US/09/167,647
CURRENT FILING DATE: 1998-10-06
EARLIER APPLICATION NUMBER: 08/479,755
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
US-09-167-647-7
Query Match 44.0%; Score 51; DB 3; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 KGSWYSMRKMSMKIRPPFPQ 20


```
; CURRENT FILING DATE: 1998-10-06
; EARLIER APPLICATION NUMBER: 08/479,755
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-167-647-1

Query Match      44.0%; Score 51; DB 3; Length 236;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRPFPPQ 20
Db      217 RGADYSLRAVRMKIRPLVTQ 236

RESULT 36
US-09-167-647-2
; Sequence 2, Application US/09167647
; Patent No. 6025476
; GENERAL INFORMATION:
; APPLICANT: Grieninge, Gerd
; APPLICANT: Fu, Yiping
; APPLICANT: Cao, Yan
; APPLICANT: Ahadi, Mohamad Zaher
; APPLICANT: Kudryk, Bohdan J.
; TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
; FILE REFERENCE: Seq.ID #1 - 7 454-7 DIV
; CURRENT APPLICATION NUMBER: US/09/167,647
; CURRENT FILING DATE: 1998-10-06
; EARLIER APPLICATION NUMBER: 08/479,755
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: PAPIO SP.
US-09-167-647-2

Query Match      44.0%; Score 51; DB 3; Length 236;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRPFPPQ 20
Db      217 RGADYSLRAVRMKIRPLVTQ 236

RESULT 37
US-09-167-647-4
; Sequence 4, Application US/09167647
; Patent No. 6025476
; GENERAL INFORMATION:
; APPLICANT: Grieninge, Gerd
; APPLICANT: Fu, Yiping
; APPLICANT: Cao, Yan
; APPLICANT: Ahadi, Mohamad Zaher
; APPLICANT: Kudryk, Bohdan J.
; TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
; FILE REFERENCE: Seq.ID #1 - 7 454-7 DIV
; CURRENT APPLICATION NUMBER: US/09/167,647
; CURRENT FILING DATE: 1998-10-06
; EARLIER APPLICATION NUMBER: 08/479,755
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: LEPORIDAE SP.
US-09-167-647-4

Query Match      44.0%; Score 51; DB 3; Length 236;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRPFPPQ 20
Db      217 RGADYSLRAVRMKIRPLVTQ 236

RESULT 38
US-09-373-157-2
; Sequence 2, Application US/09373157
; Patent No. 6418963
; GENERAL INFORMATION:
; APPLICANT: Grieninge, Gerd
; APPLICANT: Applegate, Dianne
; APPLICANT: Stoike-Steben, Lara
; TITLE OF INVENTION: NOVEL CLEAVED FRAGMENTS OF FIBRINOGEN
; FILE REFERENCE: Sequence ID No. 6418963. 1-7 for 454-24
; Patent No. 6418963
; CURRENT APPLICATION NUMBER: US/09/373,157
; CURRENT FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-157-2

Query Match      44.0%; Score 51; DB 4; Length 236;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRPFPPQ 20
Db      217 RGADYSLRAVRMKIRPLVTQ 236

RESULT 39
US-09-373-157-1
; Sequence 1, Application US/09373157
; Patent No. 6418963
; GENERAL INFORMATION:
; APPLICANT: Grieninge, Gerd
; APPLICANT: Applegate, Dianne
; APPLICANT: Stoike-Steben, Lara
; TITLE OF INVENTION: NOVEL CLEAVED FRAGMENTS OF FIBRINOGEN
; FILE REFERENCE: Sequence ID No. 6418963. 1-7 for 454-24
; Patent No. 6418963
; CURRENT APPLICATION NUMBER: US/09/373,157
; CURRENT FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-157-1

Query Match      44.0%; Score 51; DB 4; Length 251;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KGSWYSMRKMSMKIRPFPPQ 20
Db      232 RGADYSLRAVRMKIRPLVTQ 251
```

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RESULT 40
US-09-373-157-4
; Sequence 4, Application US/09373157
; Patent No. 6416963
; GENERAL INFORMATION:
; APPLICANT: Grieninger, Gerd
; APPLICANT: Grieninger, Dianne
; APPLICANT: Stoike-Steben, Lara
; TITLE OF INVENTION: NOVEL CLEAVED FRAGMENTS OF FIBRINOGEN
; FILE REFERENCE: Sequence ID No. 6416963. 1-7 for 454-24
; Patent No. 6416963
; CURRENT FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-157-4
Query Match 44.0%; Score 51; DB 4; Length 847;
Best Local Similarity 50.0%; Pred. No. 4.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSKIRPFPPQ 20
DB 828 RGADYSLRVVRMKIRPLVLTQ 847

RESULT 41
US-07-654-839-9
; Sequence 9, Application US/07654839
; Patent No. 5372933
; GENERAL INFORMATION:
; APPLICANT: Zamarron, Concepcion
; APPLICANT: Plow, Edward F
; APPLICANT: Ginsberg, Mark H
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST
; TITLE OF INVENTION: RECEPTOR-INDUCED BINDING SITES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5372933th Torrey Pines Road., Suite 220,
; STREET: Mail Drop tPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/654,839
; FILING DATE: 19910213
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252,753
; FILING DATE: 03-OCT-1988
; PRIOR APPLICATION NUMBER: US 07/415,029
; FILING DATE: 29-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Bingham, Douglas A
; REGISTRATION NUMBER: 32,457
; REFERENCE/DOCKET NUMBER: SCRO367P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-6312
; TELEFAX: 619-554-2937
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-07-654-839-5
Query Match 40.5%; Score 47; DB 1; Length 19;
Best Local Similarity 69.2%; Pred. No. 0.32;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 YSMRKMMSKIRPF 17
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-07-654-839-9
Query Match 41.4%; Score 48; DB 1; Length 13;
Best Local Similarity 61.5%; Pred. No. 0.15;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KGSWYSMRKMSK 13
DB 1 KGRWYSMKTKTK 13

RESULT 42
US-07-654-839-5
; Sequence 5, Application US/07654839
; Patent No. 5372933
; GENERAL INFORMATION:
; APPLICANT: Zamarron, Concepcion
; APPLICANT: Plow, Edward F
; APPLICANT: Ginsberg, Mark H
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST
; TITLE OF INVENTION: RECEPTOR-INDUCED BINDING SITES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5372933th Torrey Pines Road., Suite 220,
; STREET: Mail Drop tPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/654,839
; FILING DATE: 19910213
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252,753
; FILING DATE: 03-OCT-1988
; PRIOR APPLICATION NUMBER: US 07/415,029
; FILING DATE: 29-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Bingham, Douglas A
; REGISTRATION NUMBER: 32,457
; REFERENCE/DOCKET NUMBER: SCRO367P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-6312
; TELEFAX: 619-554-2937
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-07-654-839-5
Query Match 40.5%; Score 47; DB 1; Length 19;
Best Local Similarity 69.2%; Pred. No. 0.32;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 YSMRKMMSKIRPF 17
```

Db 1 YSMKTKTKIIPF 13
|||:|:|:|

RESULT 43

US-08-960-507-20
; Sequence 20, Application US/08960507
; Patent No. 6057435

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130p1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-960-507-20
Query Match 40.5%; Score 47; DB 3; Length 286;
Best Local Similarity 56.2%; Pred. No. 6;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRP 16
|||:|:|:|

Db 268 KSGYSLKATTTMIRP 283

RESULT 44

US-09-136-801-20
; Sequence 20, Application US/09136801
; Patent No. 6413770

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

SEQUENCE CHARACTERISTICS:

LENGTH: 286
TYPE: Amino Acid
TOPOLOGY: Linear

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 286

TYPE: Amino Acid

TOPOLOGY: Linear

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,801

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-136-801-20

Query Match 40.5%; Score 47; DB 4; Length 286;
Best Local Similarity 56.2%; Pred. No. 6;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRP 16

|||:|:|:|

Db 268 KSGYSLKATTTMIRP 283

RESULT 45

US-09-202-088A-20
; Sequence 20, Application US/09202088A
; Patent No. 6551822

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: TIE LIGAND HOMOLOGUES
FILE REFERENCE: P1130P3US
CURRENT APPLICATION NUMBER: US/09/202,088A
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 20

LENGTH: 286

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-202-088A-20

Query Match 40.5%; Score 47; DB 4; Length 286;
Best Local Similarity 56.2%; Pred. No. 6;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRP 16

|||:|:|:|

Db 268 KSGYSLKATTTMIRP 283

RESULT 46

US-09-134-001C-4890
; Sequence 4890, Application US/09134001C

APPLICATION NUMBER: US/09/136.828
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130R1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-828-6

Query Match 40.5%; Score 47; DB 3; Length 470;
Best Local Similarity 56.2%; Pred. No. 10;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRP 16
Db 452 RGGAYSLRKAAMLIRP 467

RESULT 50

US-09-332-928A-6
Sequence 6, Application US/09332928A
Patent No. 6368853
GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/332.928A
FILING DATE: 14-Jun-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/933,821
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-332-928A-6

Query Match 40.5%; Score 47; DB 3; Length 470;
Best Local Similarity 56.2%; Pred. No. 10;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KGSWYSMRKMSMKIRP 16
Db 452 RGGAYSLRKAAMLIRP 467
Search completed: January 18, 2005, 11:19:18
Job time : 40 secs

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